

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 27, 2005, 21:56:48 ; Search time 174 Seconds  
(without alignments)  
597,426 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 1058

Sequence: 1 MSEBIISVSDRFLSLIEH.....SSSSSSSSSENSGCRKKRY 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1058	100.0	203	2 Q9LDB6	Q9LDB6 catharanthu
2	382	36.1	210	2 Q9LEW6	Q9LEW6 catharanthu
3	358	33.8	226	2 Q8L9K1	Q8L9K1 arabidopsis
4	356.5	33.7	226	2 Q22167	Q22167 arabidopsis
5	356	33.6	202	2 Q8LBR3	Q8LBR3 glycine max
6	353	33.4	236	2 Q40476	Q40476 nicotiana t
7	345	32.6	282	2 Q9M4Y9	Q9M4Y9 mesembryant
8	339	32.0	237	2 Q9LW50	Q9LW50 nicotiana s
9	338	31.9	243	1 ERF2_ARATH	ERF2_ARATH
10	336	31.8	243	2 Q8LBU9	Q8LBU9 arabidopsis
11	333	31.5	233	2 Q40479	Q40479 arabidopsis
12	332.5	31.4	203	2 Q82447	Q82447 nicotiana t
13	330.5	31.2	244	2 Q84XB3	Q84XB3 lycopersico
14	328.5	31.0	234	2 Q04680	Q04680 lycopersico
15	324	30.6	268	1 ERF1_ARATH	ERF1_ARATH
16	323.5	30.6	235	2 Q9SE77	Q9SE77 matricaria
17	322.5	30.5	318	2 Q7XSD3	Q7XSD3 oryza sativ
18	322	30.4	328	2 Q7XU93	Q7XU93 oryza sativ
19	316.5	29.9	318	2 Q7XU94	Q7XU94 oryza sativ
20	306	28.9	303	2 Q949D4	Q949D4 oryza sativ
21	306	28.9	303	2 Q6H7H6	Q6H7H6 oryza sativ
22	296	28.0	201	2 Q84XB0	Q84XB0 lycopersico
23	296	28.0	345	2 Q949D2	Q949D2 oryza sativ
24	296	28.0	345	2 Q7XAD6	Q7XAD6 oryza sativ
25	292	27.6	344	2 Q6H6I3	Q6H6I3 oryza sativ
26	288	27.1	201	2 Q8LBD4	Q8LBD4 arabidopsis
27	286.5	27.1	244	2 Q9LND1	Q9LND1 arabidopsis
28	285.5	27.0	165	2 Q75UJ5	Q75UJ5 cucumis mel
29	285.5	27.0	201	2 Q9FKG2	Q9FKG2 arabidopsis
30	283.5	26.8	207	2 Q6V5B8	Q6V5B8 arabidopsis
31	282.5	26.7	207	2 Q6V5G9	Q6V5G9 arabidopsis

32	282.5	26.7	207	2 Q9LY05	Q9LY05 arabidopsis
33	282	26.7	206	2 Q6V5J8	Q6V5J8 brassica ol
34	281.5	26.6	207	2 Q6V5D3	Q6V5D3 olmarabido
35	277.5	26.2	218	2 Q6V5I2	Q6V5I2 sisymbrium
36	276.5	26.1	208	2 Q6WEP6	Q6WEP6 boechera dr
37	276	26.1	204	2 Q6V5F2	Q6V5F2 capsella ru
38	271.5	25.7	244	2 Q6Q4I4	Q6Q4I4 lycopersico
39	271	25.6	273	2 Q7X649	Q7X649 oryza sativ
40	271	25.6	273	2 Q9AQU3	Q9AQU3 oryza sativ
41	268	25.3	139	2 Q9LTC5	Q9LTC5 arabidopsis
42	268	25.3	198	2 Q6L4M2	Q6L4M2 oryza sativ
43	267.5	25.3	131	2 Q9L5X0	Q9L5X0 arabidopsis
44	266	25.1	161	1 PTIS LYCES	PTIS LYCES
45	265.5	25.1	268	2 Q9S2D6	Q9S2D6 arabidopsis

## ALIGNMENTS

RESULT 1					
Q9LDB6	PRELIMINARY;	PRT;	203 AA.		
AC Q9LDB6					
DT 01-OCT-2000 (T-EMBLrel. 15, Created)					
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)					
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)					
DE AP2-domain DNA-binding protein.					
GN Name=orca3;					
OS Catharanthus roseus (Rosa periwinkle) (Madagascar periwinkle).					
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;					
OC lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae;					
OC Catharanthus.					
OX NCBI_TaxID=4058;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN-G don: TISSUE=Root;					
RX MEDLINE=20355201; PubMed=10894776; DOI=10.1126/science.289.5477.295;					
RA van der Fits L., Memelink J.;					
RT "ORCA3, a jasmonate-responsive transcriptional regulator of plant					
RT primary and secondary metabolism.";					
RL Science 289:295-297(2000).					
DR EMBL; AJ251250; CAB96900.1; -.					
DR EMBL; AJ251249; CAB96899.1; -.					
DR HSSP; O80337; ZGCC.					
DR TRANSFAC; T04751; -.					
DR GO; GO:0005634; C:nucleus; IEA.					
DR GO; GO:0003700; P:transcription factor activity; IEA.					
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.					
DR InterPro; IPR001471; TF_ERF.					
DR PRINTS; PR00367; ETHRSPELEMT.					
DR Prodom; PD001423; TF_ERF.1.					
DR SMART; SM00380; AP2; 1.					
KW DNA-binding					
SQ SEQUENCE 203 AA; 22322 MW; CEE84C274312A601 CRC64;					
Query Match					
100.0%; Score 1058; DB 2; Length 203;					
Best Local Similarity 100.0%; Pred. No. 3.4e-82;					
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 MSEBIISVSDRFLSLIEHLLSDNDDSSSELTSTRENMWERFPADFLNWSGSEIQKGS	60			
DB	1 MSEBIISVSDRFLSLIEHLLSDNDDSSSELTSTRENMWERFPADFLNWSGSEIQKGS	60			
QY	61 PSSESQCSNMAESCOEDSVVGTPEAAAGGCGCKDMNRYKGVRRPMPGFAAEIDPPK	120			
DB	61 PSSESQCSNMAESCOEDSVVGTPEAAAGGCGCKDMNRYKGVRRPMPGFAAEIDPPK	120			
QY	121 KSGRIWLTGTYEPEDAAALAYDAAAFMRGAKARLNPFLIGSNISGPVAVNPKRPPAE	180			
DB	121 KSGRIWLTGTYEPEDAAALAYDAAAFMRGAKARLNPFLIGSNISGPVAVNPKRPPAE	180			
QY	181 STTSSSSSSSENSGCRKKRY 203				

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Db      181 STTSSSSSSSSSSSGRKKRY 203
      |||
RESULT 2
Q9LEH6 PRELIMINARY; PRT; 210 AA.
ID Q9LEH6
AC Q9LEH6;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE AP2-domain DNA-binding protein.
GN Name=orca2;
OS Cathartus roseus (Rose periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Apocynaceae; Rauvolfioideae; Vincaceae;
OC Cathartus.
NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9380162; PubMed=10449411; DOI=10.1093/emboj/18.16.4455;
RA Menke F.L.H., Champion A., Kijne J.W., Memelink J.;
RT "A novel jasmonate- and elicitor-responsive element in the periwinkle
RT secondary metabolite biosynthetic gene Ser interacts with a jasmonate-
RT and elicitor-inducible AP2-domain transcription factor, ORCA2.";
RL EMBL J. 18.4455-4463(1999).
DR EMBL; AJ238740; CAB93940.1; -.
DR HSSP; O80337; ZGCC.
DR TRANSFAC; T04749; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003555; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001471; TF_ERF.
DR PRINTS; PR00367; ETHRSPELEMT.
DR ProDom; PD001423; TF_ERF.1.
DR SMART; SM00380; AP2; 1.
DR DNA-binding.
KW SMART-binding.
SQ SEQUENCE 210 AA; 24021 MW; 017DF088F713CE38 CRC64;

Query Match 36.1%; Score 382; DB 2; Length 210;
Best Local Similarity 43.6%; Pred. No. 1.4e-24;
Matches 88; Conservative 27; Mismatches 35; Indels 52; Gaps 8;

QY 12 FLSLIEBHLSDSSSELTSTENBEIFADP-----LMSGSEIQKSGSPSSS 65
DB 14 FLPLVDYDFLNNDP-----FSEIFDFNANYNTSTSD-NFSGQFMEN 60
QY 66 COS---NSMAESC-----QEDSVVGP-PEAAGGCG--- 93
DB 61 CEETISPNYASELSIITIDIFKODNYDEVAGEEELITPTSRGGGGGCGEORS 120
QY 94 SKDMRYKGVRRRPMWKPFAEIRDPKKGSRIMLGTETPEDDALAYDAAMMGAKAR 153
DB 121 NEEWIMYRGVRRRPMWKPFAEIRDPKKGSRIMLGTETPEDDALAYDAAMMGAKAR 180
QY 154 LNFPHLIGNSIGPVRVPRKR 175
DB 181 LNFPHLIGS-ANAPVAVSPRR 201

RESULT 3
Q8L9K1 PRELIMINARY; PRT; 226 AA.
ID Q8L9K1
AC Q8L9K1;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Putative ethylene response element binding protein (EREBP).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

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OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volkovsky N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY088387; AM65925.1; -.
DR HSSP; O80337; ZGCC.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003555; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000977; DNA_ligase.
DR PRINTS; PR00367; ETHRSPELEMT.
DR ProDom; PD001423; TF_ERF.1.
DR SMART; SM00380; AP2; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
SQ SEQUENCE 226 AA; 25367 MW; C3F80438CF19D80 CRC64;

Query Match 33.8%; Score 358; DB 2; Length 226;
Best Local Similarity 44.8%; Pred. No. 1.7e-22;
Matches 79; Conservative 24; Mismatches 55; Indels 18; Gaps 5;

QY 21 LLSNDSSELTSTENBEIFADFLMWSGSEIQKSGSPSSSCQSNMAESCQEDSV 80
DB 26 ILNDMSDPLSLVDDSD-----MAIYTLRAVASAMTPSPVPTS-----PAEDK- 73
QY 81 VGTPEPAAGGCGS--KDMRYKGVRRRPMWKPFAEIRDPKKGSRIMLGTETPEDAL 138
DB 74 ---PPATKASGSHAPQKGQYRGVRRRPMWKPFAEIRDPKKGARVWLGTETPEDAAV 130
QY 139 AYDAAMMGAKARLNFPHLIGNSIGPVRVPRKRPAEPETSSSSSSSEN 194
DB 131 AYDAARQLGSGXAKLNFPHLIGSCXYEPVRIPIRRRSP-EPSVSDQLTSEQRES 165

RESULT 4
Q22167 PRELIMINARY; PRT; 226 AA.
ID Q22167
AC Q22167;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Putative ethylene response element binding protein (Putative ethylene
DE response element binding protein; EREBP).
GN Name=At2g44840;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
RA Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

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Query	Best Match	Similarity	41.3%	Score	356	DB	22	Length	202
Matches	83	Conservative	29	Mismatches	35	Indels	34	Gaps	5
Qy	9	SDFRFLSLIEHLLTNSDSSSELTSTENWEEIFADFLMWSGEIOKRSPSSSCQS	68	8	SDFAPFLSYQYVLGHDSINLMSETHQAASH--DFPSD-----	PKCGGDS	51		
Dy	69	NSMAESCQDSVY---GTPEPAAAGCGCSKDMNRKCYVRPPNGKFAAEIRDPKKGSR	12	52	GNIAFPSESDATVAVRADHAPF-----TWKHYRQVRRRRPNGKFAAEIRDPKKGAR	10			
Qy	125	IMVGTETEPEDAAIYDAAEFMRGAKALNPPIHSGN-----ISGPRVVRPRRPAEP	18	102	VIMGTGYDTEERKALAYDKAFAFRGQAKALNPHLIDNSDELSEPMVMTTSKRSLLEI	16			
Dy	181	STTSSSSSSSSSENSGGRKR	201	162	SSPSSSCSDSSSESGCTKRK	182			

RESULT 6

Q040476 PRELIMINARY; PRT; 236 AA.

AC Q040476;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE ERP1.

OS Nicotiana tabacum (Common tobacco).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Nicotiana.

OC NCBI\_TaxID=4097;

OX [1]

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BY4; TISSUE=Leaf;

RA Suzuki K., Suzuki N., Ohme-Takagi M., Shinohi H.;

RT "Immediate early induction of mRNAs for ethylene-responsive transcription factors in tobacco leaf strips after cutting.";

RL Plant J. 15:657-665(1998).

DR EMBL; D38123; BAA07321.1; -.

DR PIR; T02432; T02432.

DR HSSP; O80337; 2GCC.

DR TRASPAC; T02653; -.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR001471; TF\_ERF.

DR PRINTS; PR00367; ETHRSPLEMMT.

DR ProDom; PD001423; TF\_ERF.1.

DR SMART; SM00380; AP2; 1.

DR PROSITE; PS00697; DNA\_LIGASE\_A1; UNKNOWN1.

DR SEQUENCE 202 AA; 22467 MW; 1B875A6EB2AVD56D CRC64;

Query Match 33.4%; Score 353; DB 2; Length 236;  
 Best Local Similarity 45.3%; Pred. No. 4.9e-22;  
 Matches 81; Conservative 20; Mismatches 50; Indels 28; Gaps 6;

QY 27 DSSSLSTTEENWEIIFADFLN--WSSSEIOKRGSPSSSCQSNMAESCOEDSVGTP 84  
 DB 46 DSEDMVIYI-----LTKDALNVGSPSPNF-SAGEVXSEQ-----REEIVVSP 88  
 QY 85 PEAAGCGCKDMNR-YKGVRRRPMGKFAAIRDPKKGSRIWLTGYETPEDALAYDAA 143  
 DB 89 AETTAAPAELEPRGRHYRGRVRRRPMGKFAAIRDPAKNARVWLTGYETDEDAIAYDKA 148  
 QY 144 AFNRGAKARLNPPLHIGSNISGVRVNPVKRFPAPBPTSSSSSSSSSSSSSGRKKR 202  
 DB 149 AYMRGSKALNLPFHRIGLNEPEPVVTAKRASPEP-----ASSSENSPRRRK 199

## RESULT 7

Q9M4Y9 PRELIMINARY; PRT; 282 AA.  
 AC Q9M4Y9;  
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DE AP2-related transcription factor (Ethylene responsive protein).  
 GN Name:CDBP; Synonyms:EREB;  
 OS Mesembryanthemum crystallinum (Common ice plant).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Alzooceae; Mesembryanthemum.  
 NC NCB1\_TaxID=3544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RA Scharte J., Baur B.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Hou Y.-X., Cheng X.-G., Zhang J.;  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP245119; AAP63205.1; -;  
 DR EMBL; AF537265; AAP80810.1; -;  
 DR HSSP; 080337; 2GCC.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR PRINTS; PRO0367; ETHRSPELEMT.  
 DR ProDom; PD001423; TF\_ERF.1.  
 DR SMART; SM00380; AP2.1.  
 SQ SEQUENCE 282 AA; 30011 MW; 617C32009C535B29 CRC64;

Query Match 32.6%; Score 345; DB 2; Length 282;  
 Best Local Similarity 40.5%; Pred. No. 2.9e-21;  
 Matches 96; Conservative 22; Mismatches 63; Indels 56; Gaps 10;

QY 9 SDRFLSLTEETHLSD-----NSDDSS-----SELSTSTEEN 39  
 DB 9 SDRAVLESTRRLLEEDWDPAAGAPATTGSGPYTHRNSSFSLLYPLCLTNWGBLPKEDD 68  
 QY 40 WEIIF-----ADFLNW--SGSEIOKRGSPSSSCQSNMAESCOEDSVGTP-PEAA 88  
 DB 69 SEDMWLFGLVRLADVHVGMSQSGSE-SGSGSPAPVTVKPEPV-----DSPVSPAPRV 121  
 QY 89 AGC-----GCKDMNRKYGVRRRPMGKFAAIRDPKKGSRIWLTGYETPEDALAYDAA 143  
 DB 122 AGCEAEVAAAPARGKHYRGRVRRRPMGKFAAIRDPAKNARVWLTGYETDEDAIAYDRA 181  
 QY 144 AFNRGAKARLNPPLHIGSNISGVRVNPVKRFPAPBPTSSSSSSSSSSSSSGRKKR 200  
 DB 182 AFMRGSKALNLPPLRVNSGPEPVRITKRSRP-ERSVSSSSSSSSSASPGR--RKK 234

## RESULT 8

Q9LM50 PRELIMINARY; PRT; 237 AA.  
 AC Q9LM50;  
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)  
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Ethylene-responsive element binding factor.  
 GN Name=erf2;  
 OS Nicotiana glauca (Wood tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Nicotiana.  
 NC NCB1\_TaxID=4096;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20399450; PubMed=10945353;  
 RA Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;  
 RT "Characterization of gene expression of NERFs, transcription factors  
 of basic PR genes from Nicotiana glauca.";  
 RL Plant Cell Physiol. 41:817-824(2000).  
 DR EMBL; AB016264; BAA97122.1; -;  
 DR HSSP; 080337; 2GCC.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR PRINTS; PRO0367; ETHRSPELEMT.  
 DR ProDom; PD001423; TF\_ERF.1.  
 DR SMART; SM00380; AP2.1.  
 SQ SEQUENCE 237 AA; 26243 MW; 01BC3EEB51E46298 CRC64;

Query Match 32.0%; Score 339; DB 2; Length 237;  
 Best Local Similarity 44.3%; Pred. No. 7.7e-21;  
 Matches 82; Conservative 23; Mismatches 54; Indels 26; Gaps 7;

QY 24 DNSDDSS-----SSELTSTEENWEIIFADFLNWSGSEIOKRGSPSSSCQSNMAESCOE 77  
 DB 37 DSEDMVIYIGLSDALTY--GWTP-----FNLTSTEI--KAPFREIPATSPVPS--- 83  
 QY 78 DSVYGTPEEAAGCGCKDMNRKYGVRRRPMGKFAAIRDPKKGSRIWLTGYETPEDA 137  
 DB 84 ---VAAPAEITTTAAVVPKGRHYRGRVRRRPMGKFAAIRDPAKNARVWLTGYETAEAA 140  
 QY 138 LAYDAAFNRGAKARLNPPLHIGSNISGVRVNPVKRFPAPBPTSSSSSSSSSSSGRKKR 197  
 DB 141 LAYDKAAYRRGSKALNLPFHRIGLNEPEPVVTAKRASPEP---ASSISIPASNSLP 196

QY 198 RKKRR 202  
 DB 197 KRRRK 201

## RESULT 9

EF2\_ARATH STANDARD; PRT; 243 AA.  
 AC EF2\_ARATH;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ethylene responsive element binding factor 2 (AtERF2).  
 GN Name=ERF2; Synonyms=ERF-2; OrderedlocusNames=At5g47220;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NC NCB1\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20181733; PubMed=10715325;  
 RA Fujimoto S.Y., Ohta M., Ueul A., Ohme-Takagi M.;



Query	Best Local Match	Similarity	Score	DB 2	Length	243
Db	9	SDVALLSITRHLGGGE---	31.8*	39.4*	Pred. No. 1.4e-20,	Matches 85; Conservative 29; Mismatches 70; Indels 32; Gaps 6
Qy	9	SDRFLLELIEHLLSDNSDSSSELTTEENWEEIFADFLNWSSEIQRGS-----	60			
Db	9	SDVALLSITRHLGGGE---	31.8*	39.4*	Pred. No. 1.4e-20,	Matches 85; Conservative 29; Mismatches 70; Indels 32; Gaps 6
Qy	61	-PSESCQSNMAESQCED-----	SVGTPEEAAAGCGSKDMNRYKGVRR	106		
Db	64	LKQDFHPTDSSDLSCLFDPFAVKEPTENFTNEMAEKPKKAIPTETAVKAKHYRGVQR	123			
Qy	107	PMGEAAEIDDPKKSGRIWLGTEPEPDALAVDAAFNNRGAKARLNPHLGSIISG	166			
Db	124	PMGEAAEIDDPKKSGRIWLGTEPEPDALAVDAAFNNRGAKARLNPHLGSIISG	183			
Qy	167	PVRVNPKRFPAPBPTTSSSSSSSSSSSGGRKKR	202			
Db	184	PVRITSKR---SSSSSSSSSSSTSSSEN-CKLKR	214			

RESULT 11

Q040479 PRELIMINARY; PRT; 233 AA.

AC Q040479; 040479; PRELIMINARY; PRT; 233 AA.

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Eclylene-responsive element binding protein.

GN Name=ERBP-2.

OS Nicotiana tabacum (Common tobacco).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.

OC NCBI\_TaxID=4097;

OX NCBI\_TaxID=4097;

PN [1]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

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RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

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RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

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RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Flavell R., Flavell R., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome annotation."

RA Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).

RP [2]

RP SEQUENCE FROM N.A.

RA Bover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RA Haas B.J., Volfovsky N., Town C.D., Troukhan M.,

RC STRAIN=BY4; TISSUE=Leaf;  
 RA Suzuki K., Suzuki N., Ohme-Takagi M., Shinshi H.;  
 RT "Immediate early induction of mRNAs for ethylene-responsive  
 transactivator factors in tobacco leaf strips after cutting."  
 RL Plant J. 15:657-665(1998).  
 DR EMBL: D8126; BAA07324.1; -  
 DR PIR: T02590; T02590.  
 DR HSSP: 080337; 2GCC.  
 DR TRANSFAC: T02654; -  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS: PR00367; ETHRSPLEMT.  
 DR ProDom: PD001423; TF\_ERF; 1.  
 DR SMART: SM00380; AP2; 1.  
 SQ SEQUENCE 233 AA; 25563 MW; 6CD16783582C0CB5 CRC64;

Query Match 31.5%; Score 333; DB 2; Length 233;  
 Best Local Similarity 54.9%; Pred. No. 2.4e-20;  
 Matches 67; Conservative 16; Mismatches 35; Indels 4; Gaps 2;

QY 81 VCTPPPAAGGCGCKDMNRKYGRRRPCKFAAEIRDPKKGSRIWLGTYETPEDALAY 140  
 DB 80 VAPPAETTAQAVVPKGRHRYGVROKPPWCKFAAEIRDPKNGARVWLGTYTEAEBAALAY 139  
 QY 141 DAAAFMRGAKARLNPPLIGSNISGVRVNRKPPAPSPSTSSSSSSSSSSSSSGGRKK 200  
 DB 140 DKAAVMRSGKALLNPFRIGLNEPEPVATKRRSP-EP---ASSSISSALENSGPKRR 195

QY 201 RR 202  
 DB 196 RK 197

RESULT 12  
 082447 PRELIMINARY; PRT; 203 AA.  
 ID 082447;  
 AC 082447;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Ethylene response element binding protein 1 (Fragment).  
 GN Name=EREBP1;  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Nicotiana.  
 OC NCBI\_TaxID=4097;  
 RN RP SEQUENCE FROM N.A.  
 RX MEDLINE=98392433; PubMed=9725022;  
 RA Horvath D.M., Huang D.J., Chua N.H.;  
 RT "Four classes of salicylate-induced tobacco genes."  
 RL Mol. Plant Microbe Interact. 11:895-905(1998).  
 DR EMBL: AF057373; AAC62619.1; -  
 DR HSSP: 080337; 2GCC.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS: PR00367; ETHRSPLEMT.  
 DR ProDom: PD001423; TF\_ERF; 1.  
 DR SMART: SM00380; AP2; 1.  
 FT NON TER 1  
 SQ SEQUENCE 203 AA; 22616 MW; F62AB477B0B017DE CRC64;

Query Match 31.4%; Score 332.5; DB 2; Length 203;  
 Best Local Similarity 41.8%; Pred. No. 2.3e-20;  
 Matches 77; Conservative 20; Mismatches 50; Indels 37; Gaps 6;

QY 37 EENWEE-----IFADFLN--WGSSEIQKRGSPSSSCQNSMAESCQEDS 79  
 AC 37 EENWEE-----IFADFLN--WGSSEIQKRGSPSSSCQNSMAESCQEDS 79

DB 2 EETWSELPLKVDSEDMVIYTLIKDALNVGWSPFNE-TAGEVXSE-----LMEESE 50  
 QY 80 VCTPPPAAGGCGCKDMNR-XYGVRRPCKFAAEIRDPKKGSRIWLGTYETPEDAL 138  
 DB 51 IVSPADTTTAAPAELPRGHRYGVRRKPPWCKFAAEIRDPKNGARVWHRITETDEAL 110  
 QY 139 AYDAAFMNRGAKARLNPPLIGSNISGVRVNRKPPAPSPSTSSSSSSSSSSSSSGGR 198  
 DB 111 AYDKAAVMRSGKALLNPFRIGLNEPEPVATKRRASPEP-----ASSSENSAK 162  
 QY 199 KRR 202  
 DB 163 RRRK 166

RESULT 13  
 084XB3 PRELIMINARY; PRT; 244 AA.  
 ID 084XB3;  
 AC 084XB3;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Ethylene response factor 1.  
 GN Name=ERF1;  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Solanum.  
 OC NCBI\_TaxID=4081;  
 RN RN SEQUENCE FROM N.A.  
 RP MEDLINE=22816770; PubMed=12935902; DOI=10.1016/S0014-5793(03)00757-9;  
 RA Tournier B., Sanchez-Ballester M.T., Jones B., Peesquet E., Regad F.,  
 RA Latche A., Pech J.C., Bouzayen M.;  
 RT "New members of the tomato ERF family show specific expression pattern  
 and diverse DNA-binding capacity to the GCC box element."  
 RL FEBS Lett. 550:149-154(2003).  
 DR EMBL: AY192367; AAC034703.1; -  
 DR HSSP: 080337; 2GCC.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS: PR00367; ETHRSPLEMT.  
 DR ProDom: PD001423; TF\_ERF; 1.  
 DR SMART: SM00380; AP2; 1.  
 SQ SEQUENCE 244 AA; 27085 MW; D090818A6CE5B833 CRC64;

Query Match 31.2%; Score 330.5; DB 2; Length 244;  
 Best Local Similarity 39.2%; Pred. No. 4.2e-20;  
 Matches 78; Conservative 21; Mismatches 61; Indels 39; Gaps 4;

QY 26 SDDSSSELTSTENW-----EIRADFL-----NWSGSEIQKRGSPSS 63  
 DB 23 SSSPSSSLPCLTBSWGDLPKVNDSBDMVIYGLQDAFSGIWTPSNLTSEVRLPREET 82  
 QY 64 SSCQSNMASSCQDSDVVTPEAAGCGCKDMNRKYGRRRPCKFAAEIRDPKKGS 123  
 DB 83 EPANSTSVS-----PPTVAPALAQPKGRHRYGVROKPPWCKFAAEIRDPKNGA 130  
 QY 124 RIMLGTYETPEDALAYDAAAFMRGAKARLNPPLIGSNISGVRVNRKPPAPSPSTT 183  
 DB 131 RVMLGTYESAEBEALAYGKAAPMRGKALNLPFRIGLNEPEPVATVGRRL-----SE 185  
 QY 184 SSSSSSSSSSSSGGRKKR 202  
 DB 186 SASSSVSSASBSGSPKRR 204

RESULT 14  
 004680 PRELIMINARY; PRT; 234 AA.  
 ID 004680  
 AC 004680;

DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Pe14 (Fragment).  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Solanum.  
 NC NCB1\_TaxID=4081;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97537308; PubMed=9214637; DOI=10.1093/emboj/16.11.3207;  
 RA Zhou J., Tang X., Martin G.B.;  
 RT "The Pto kinase conferring resistance to tomato bacterial speck  
 disease interacts with proteins that bind a cis-element of  
 pathogenesis-related genes".  
 RT EMBO J. 16:3207-3218(1997).  
 RL (2)  
 RN SEQUENCE FROM N.A.  
 RA Zhou J., Tang X., Martin G.B.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U89255; AAC50047.1; -  
 DR PIR; T07686; T07686.  
 DR HSSP; 080337; 2GCC.  
 DR TRASNFAc; T04715; -  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; E:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR INTERP; IPR001471; TF\_ERF.  
 DR PRINTS; PR00367; ETRSPLEMMT.  
 DR Prodom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 FT NON\_TER 234 234  
 SQ SEQUENCE 234 AA; 26001 MW; FC96F5690F08AAA4A CRC64;  
 QY Best Match 31.0%; Score 328.5; DB 2; Length 234;  
 QY Best local Similarity 47.1%; Pred. No. 5.9e-20;  
 QY Matches 73; Conservative 18; Mismatches 43; Indels 21; Gaps 5;  
 Db 49 NMSGSEIQRKSPSSSCSNMAESCOEDSVVGTPEEAAAGGCSKDMNR-YKGVARRP 107  
 65 NFFAGGV--KSEPRE-----IESSPES--PSPETTTAAAPAEKGRHYRGVQRQRP 113  
 QY 108 WGFPAEIDPKKKGRIMVLTETPEDAALVDAANFNKGAARINPFLIGSNISGP 167  
 114 WGFPAEIRDPANRGARVWLTETPEEAAIADKAAVRRMSKAHLNPHRIGLNEPEP 173  
 QY 168 VRVNPKRFPAPSPSTSSSSSSSSSSSGGRKKRR 202  
 Db 174 VRVTAKRASPEP-----ASSSGSGMKRRR 199  
 RESULT 15  
 ERFL\_ARATH STANDARD; PRT; 268 AA.  
 AC 080337; Q93236; Q9SUK1;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Ethylene responsive element binding factor 1 (AtERF1) (ERESP-2  
 DE protein).  
 GN Name:ERF1; Synonyms=ERF-1; OrderedLocusNames=At4g17500;  
 GN ORFNames=D14785W;  
 GN Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
 NC NCB1\_TaxID=5702;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. C24;  
 RX MEDLINE=20181733; PubMed=10715325;  
 RA Fujimoto S.Y., Ohta M., Usui A., Shinshi H., Ohme-Takagi M.;

RT "Arabidopsis ethylene responsive element binding factors act as  
 RT transcriptional activators or repressors of GCC box mediated gene  
 RT expression.";  
 RT Plant Cell 12:393-404(2000).  
 RL (2)  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=98121113; PubMed=9461215; DOI=10.1038/35140;  
 RA Bevan M., Bancroft I., Bent E., Love K., Goodman H.M., Dean C.,  
 RA Bergkamp R., Dirks W., van Staveren M., Stiekema W., Drost L.,  
 RA Ridley P., Hudson S.-A., Patel K., Murphy G., Piffanelli P.,  
 RA Piavandi E., Obermaier B., Hilbert H., Duesterhoeft A., Moores T.,  
 RA Gielen J., Villarroel R., De Clercq R., van Montagu M., Lecharny A.,  
 RA Aubourg S., Gy I., Kreis M., Leo N., Kavanagh T., Hempel S.,  
 RA Kotter P., Entian K.-D., Rieger M., Schaefer M., Funk B.,  
 RA Mueller-Auer S., Silvey M., James R., Montfort A., Pons A.,  
 RA Puigdomenech P., Douka A., Vouklatou E., Milioni D., Hatzopoulos P.,  
 RA Piavandi E., Obermaier B., Hilbert H., Duesterhoeft A., Moores T.,  
 RA Jones J.D.G., Eneva T., Palme K., Benes V., Rechmann S., Ansoorge W.,  
 RA Cooke R., Berger C., Delseny M., Voet M., Volckaert G., Mewes H.-W.,  
 RA Klosterman S., Schueller C., Chalwatzis N.;  
 RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of  
 RT Arabidopsis thaliana.";  
 RL Nature 391:485-486(1998).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;  
 RA Mohr K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,  
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,  
 RA Harris B., Ansoorge W., Brandt P., Griwell L.A., Rieger M.,  
 RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,  
 RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheim T.,  
 RA Reichert B., Portelelle D., Perez-Alonso M., Boutry M., Bancroft I.,  
 RA Vos P., Hohenseil J., Zimmermann W., Wedler H., Ridley P.,  
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,  
 RA van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,  
 RA Braeken H., Weltjens I., Voet M., Baetsens I., Aert R., Defoor E.,  
 RA Weltenegeger T., Botte G., Rampsperger U., Hilbert H., Braun M.,  
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirks W.,  
 RA Moolman P., Klein lankhorst R., Rose M., Hauf J., Koetter P.,  
 RA Bernieris S., Hempel S., Feldpausch M., Lambirth S., Van den Daele H.,  
 RA de Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,  
 RA van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,  
 RA Clark L., Doggett J., Hall S., Kay W., Lennard N., Mcley K., Mayes R.,  
 RA Peltett A., Rajadream M.A., Lyne M., Benes V., Rechmann S.,  
 RA Borkova D., Blocker H., Scharfe M., Grimm M., Loehert T.-H.,  
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fartmann B., Granderath K., Danner D., Herzi A.,  
 RA Neumann S., Argitrou A., Vitale D., Liguori R., Piravandi E.,  
 RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,  
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,  
 RA Chefor F., Cooke R., Berger C., Montfort A., Casacuberta E.,  
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,  
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,  
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bieleke C.,  
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,  
 RA Zaccaria P., Bevan M., Wilson R.K., de la Baulie M., Habermann K.,  
 RA Parnell L., Dehbia N., Gnoj L., Schutz K., Huang E., Siegel L.,  
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,  
 RA Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,  
 RA Latreille P., Courtney L., Clout J., Abbott A., Scott K., Johnson D.,  
 RA Mxnx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,  
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,  
 RA Nelson J., Splich J., Ryan E., Andrews S., Giesel C., Layman D.,  
 RA Du H., Ali J., Berghoff A., Jones K., Drome K., Cotton M., Joshi C.,  
 RA Antonciu B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,  
 RA Ma P., Zhong U., Preston R., Vil D., Shekher M., Matero A., Shah R.,  
 RA Swaby I.K., O'Shaughnessy A., Rodriguez W., Hoffman J., Tili S.,  
 RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodi M., Johnson A.,  
 RA Chen E., Maria M.A., Marijansen R., McCombie W.R.;  
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis  
 RT thaliana.";

RL Nature 402:769-777(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;  
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.U.,  
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Pham P.K., Cheuk R.F.,  
 RA Kaitlin-Newmann G., Liu S.X., Lam B., Sakano H., Pham P.K., Cheuk R.F.,  
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,  
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,  
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,  
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,  
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,  
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,  
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,  
 RA Satou M., Tamse R., Vayenberg M., Wallender E.K., Wong C., Yamamura Y.,  
 RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.,  
 RT "Empirical analysis of transcriptional activity in the Arabidopsis  
 RT genome.";  
 RL Science 302:842-846(2003).  
 RN [5]  
 RP STRUCTURE BY NMR OF 146-208.  
 RX MEDLINE=98409552; PubMed=9736626; DOI=10.1093/emboj/17.18.5484;  
 RA Allen M.D., Yamasaki K., Ohme-Takagi M., Tateo M., Suzuki M.,  
 RT "A novel mode of DNA recognition by a beta-sheet revealed by the  
 RT solution structure of the GCC-box binding domain in complex with  
 RT DNA.";  
 RL EMBO J. 17:5484-5496(1998).  
 RN [6]  
 RP INDUCTION.  
 RX MEDLINE=99069218; PubMed=9851977;  
 RA Solano R., Stepanova A.N., Chao Q., Ecker J.R.,  
 RT "Nuclear events in ethylene signaling: a transcriptional cascade  
 RT mediated by ETHYLENE-INSENSITIVE3 and ETHYLENE-RESPONSE-FACTOR1.";  
 RL Gene Dev. 12:3703-3714(1998).  
 CC -1- FUNCTION: transcription factor that binds to the GCC-box  
 CC pathogenesis-related promoter element.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- INDUCTION: Ethylene induction of ERF1 is completely dependent on a  
 CC functional ETHYLENE-INSENSITIVE3 (EIN3) protein.  
 CC -1- SIMILARITY: Contains 1 AP2/ERF domain.  
 CC -1- CAUTION: Ref.2 and Ref.3 sequences differ from that shown due to a  
 CC frameshift in position 44.  
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-3 is the initiator.  
 CC  
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 CC  
 DR EMBL: AB008103; BAB32418.1; ALT\_INIT.  
 DR EMBL: Z97343; CAB45963.1; ALT\_FRAME.  
 DR EMBL: AL161546; CAB78753.1; ALT\_FRAME.  
 DR EMBL: AY058174; AAL25588.1;  
 DR EMBL: AY062533; AAL32611.1;  
 DR EMBL: BT002578; AAC00938.1;  
 DR PDB: 1GCC; NMR; A=144-206.  
 DR PDB: 2GCC; NMR; @=141-210.  
 DR PDB: 3GCC; NMR; @=141-210.  
 DR TRANSFAC: T04633;  
 DR InterPro: IPR001471; TF\_ERF.  
 DR Pfam: PF00847; AP2\_1.  
 DR PRINTS: PR00367; ETRSPLELNT.  
 DR ProDom: PD001423; TF\_ERF\_1.  
 KM 3D-structure; DNA-binding; Nuclear protein; Transcription regulation.  
 FT DNA BIND 143 208 AP2/ERF.  
 SQ SEQUENCE 268 AA; 29189 MW; 0FB7839984E97B50 CRC64;

Query Match 30.6%; Score 324; DB 1; length 268;  
 Best local Similarity 36.0%; Pred. No. 1.7e-19;

Matches	91; Conservative	27; Mismatches	69; Indels	66; Gaps	9;
Oy	1 MSEELISVSDRFLSLIEHLSDN---- <td></td> <td></td> <td></td> <td>36</td>				36
Db	1 MSMTADSQSYATLLESLRRLLESEBPIILSESTASSVTQSCVTCGSIKPYVGNPFSKL				60
Oy	37 ----EENW-----EELFADFL-----NW---SGSEIQKRGSPS--SESCQSN				69
Db	61 YPCPTESWGLDPLKENDSEDMLVYGLINDAFHCGMWPSSSSSDSDRSSFPVXIEPTESF				120
Oy	70 SMAESCQEDSVGTTPPEAALAGGCGSKDMRYKGVRRRPPMGFAELRDPKKGRITWLTG				129
Db	121 AAVDSVVKKEKTSVSAAYTAAGK--HYRGVROPWGKFAELRDPAKNGARVWLTG				177
Oy	130 YETPEDAALAYDAAAFNMRGAKARLNFPHLIGSNIISGPVVRNPKRFPAPSTSSSSSS				189
Db	178 FETMEDAALAYDAAAFNMRGSRLLNFPRLRVNNGEFPDPRIRKSR-----SFS				226
Oy	190 SSSENSGGRKKR 202				
Db	227 SSNEN-GAPKKR 238				

Search completed: February 27, 2005, 22:06:06  
 Job time : 177 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 27, 2005, 21:48:28 ; Search time 163 Seconds

(without alignments)  
481.671 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 1058

Sequence: 1 MSERITVSDFRFLSLIEH.....SSSSSSSSSSSGRRKRRY 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq.16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1058	100.0	203	AA97228	Aay97228 Plant tra
2	400	37.8	227	ADG00355	Adg00355 Nicotiana
3	382	36.1	210	AA97227	Aay97227 Plant tra
4	358	33.8	212	AA924800	Aag24800 Arabidops
5	358	33.8	226	AA924799	Aag24799 Arabidops
6	357.5	33.8	183	AA924801	Aag24801 Arabidops
7	356.5	33.7	183	AA934782	Aag34782 Arabidops
8	356.5	33.7	212	AA934781	Aag34781 Arabidops
9	356.5	33.7	226	AA934780	Aag34780 Arabidops
10	356.5	33.7	226	AA934780	Aag34780 Arabidops
11	356.5	33.7	226	AA934780	Aag34780 Arabidops
12	356.5	33.7	226	AA934780	Aag34780 Arabidops
13	356.5	33.7	226	AA934780	Aag34780 Arabidops
14	356.5	33.7	226	AA934780	Aag34780 Arabidops
15	356.5	33.7	226	AA934780	Aag34780 Arabidops
16	356.5	33.7	226	AA934780	Aag34780 Arabidops
17	356.5	33.7	226	AA934780	Aag34780 Arabidops
18	356.5	33.7	226	AA934780	Aag34780 Arabidops
19	356.5	33.7	226	AA934780	Aag34780 Arabidops
20	356.5	33.7	226	AA934780	Aag34780 Arabidops
21	356.5	33.7	226	AA934780	Aag34780 Arabidops
22	356.5	33.7	226	AA934780	Aag34780 Arabidops
23	356.5	33.7	226	AA934780	Aag34780 Arabidops
24	356.5	33.7	226	AA934780	Aag34780 Arabidops
25	356.5	33.7	226	AA934780	Aag34780 Arabidops

26	324	30.6	268	AA905106	Aag05106 Arabidops
27	324	30.6	268	AA905106	Aag05106 Arabidops
28	324	30.6	268	AA905106	Aag05106 Arabidops
29	324	30.6	268	AA905106	Aag05106 Arabidops
30	324	30.6	268	AA905106	Aag05106 Arabidops
31	324	30.6	268	AA905106	Aag05106 Arabidops
32	324	30.6	268	AA905106	Aag05106 Arabidops
33	324	30.6	268	AA905106	Aag05106 Arabidops
34	324	30.6	268	AA905106	Aag05106 Arabidops
35	324	30.6	268	AA905106	Aag05106 Arabidops
36	324	30.6	268	AA905106	Aag05106 Arabidops
37	324	30.6	268	AA905106	Aag05106 Arabidops
38	324	30.6	268	AA905106	Aag05106 Arabidops
39	324	30.6	268	AA905106	Aag05106 Arabidops
40	324	30.6	268	AA905106	Aag05106 Arabidops
41	324	30.6	268	AA905106	Aag05106 Arabidops
42	324	30.6	268	AA905106	Aag05106 Arabidops
43	324	30.6	268	AA905106	Aag05106 Arabidops
44	324	30.6	268	AA905106	Aag05106 Arabidops
45	324	30.6	268	AA905106	Aag05106 Arabidops

## ALIGNMENTS

RESULT 1	AA97228	standard; protein; 203 AA.
ID	AA97228	
AC	AA97228	
XX		
DT	19-DEC-2000	(first entry)
DE	Plant transcription factor AP2 DNA-binding domain polypeptide.	
XX		
KM	AP2; transcription factor; plant metabolism; metabolite; primary;	
KW	secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;	
KW	food colouring; flavouring; fragrance; antimicrobial; pathogenic;	
KW	insecticide; gene expression; modulation.	
XX		
OS	Catharanthus roseus.	
PN	W0200046383-A2.	
XX		
PD	10-AUG-2000.	
XX		
PF	07-FEB-2000; 2000WC-NL000075.	
PR	05-FEB-1999; 99DK-00000158.	
PR	10-FEB-1999; 99US-0119388P.	
XX		
PA	(UYLE-) RIKSUNIV LEIDEN.	
PI	Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW;	
XX		
DR	WPI; 2000-499380/44.	
DR	N-PSDB; AAA53745.	
PT	Modulating level of metabolites and stress resistance in recombinant	
PT	cells for synthesis of plant metabolites such as alkaloids including	
PT	terpenoid indole alkaloids, by providing transcription factor to the	
PT	cell.	
XX		
PS	Disclosure; Page 97-98; 101pp; English.	
XX		
CC	Many plant secondary metabolites have value as pharmaceuticals, food	
CC	colourings, flavours and fragrances. Some plant secondary metabolites are	
CC	linked to plant or plant cell defence mechanisms and may confer to the	
CC	plant antimicrobial activity, protection against UV light, herbivores,	
CC	pathogens, insects and nematodes. Plant secondary metabolites such as	
CC	terpenoid indole alkaloids (TIA) represent a class of pharmaceutically	
CC	useful compounds which naturally occur in many plant species. New methods	
CC	are described which modulate the expression of one or more genes involved	

CC in the biosynthesis of plant metabolites or their precursors in plant  
CC cells. The method comprises inserting into a plant DNA-binding domain and  
CC encoding a transcription factor comprising an AP2 DNA-binding domain and  
CC by modifying the expression of that transcription factor. Transcription  
CC factors comprising an AP2 DNA-binding domain are useful as central  
CC regulators of complex metabolite pathways involving numerous target genes  
CC for such transcription factors. This means that the yield of commercially  
CC valuable metabolite compounds can be enhanced and the tolerance of plants  
CC towards exogenous stress factors can be influenced. The method is useful  
CC for modulating the level of one or more metabolites. By providing a  
CC transcription factor to the cell the level of the metabolite is enhanced  
CC by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to  
CC a cell to which the transcription factor is not provided  
XX

SQ Sequence 203 AA;

Query Match 100.0%; Score 1058; DB 3; Length 203;  
Best Local Similarity 100.0%; Pred. No. 1.6e-106;  
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSEITSVSDRFLSLIEEHLSDNSDSSSELTSTEENWEIEFADFLNWSSEIQKGS 60  
DB 1 MSSEITSVSDRFLSLIEEHLSDNSDSSSELTSTEENWEIEFADFLNWSSEIQKGS 60  
QY 61 PSSESCQSNMASESCQEDSVGTPEPAAGGCGSKDMNRKGVRRRPMWGFPAEIRDPK 120  
DB 61 PSSESCQSNMASESCQEDSVGTPEPAAGGCGSKDMNRKGVRRRPMWGFPAEIRDPK 120  
QY 121 KGRIRWLGTYETPEPDAALAYDAAAFNMRGAKARLNFPHLIGSNISGPRVNPFRKPPAP 180  
DB 121 KGRIRWLGTYETPEPDAALAYDAAAFNMRGAKARLNFPHLIGSNISGPRVNPFRKPPAP 180  
QY 181 STTSSSSSSSSSSSSSGRKKRRY 203  
DB 181 STTSSSSSSSSSSSSSGRKKRRY 203

RESULT 2

ADG00355

ID ADG00355 standard; protein; 227 AA.

XX AC ADG00355;

XX DT 26-FEB-2004 (first entry)

XX DE Nicotiana tabacum variant bright yellow protein sequence SEQ ID NO:872.

XX KW secondary metabolite modulator; biosynthesis; alkaloid; phenylpropanoid;

XX KM tobacco; Nicotiana tabacum variant bright yellow; Nicotiana tabacum BY;

XX KM plant.

XX OS Nicotiana tabacum.

XX PN WO2003097790-A2.

XX PD 27-NOV-2003.

XX PF 16-MAY-2003; 2003WO-EP050171.

XX PR 17-MAY-2002; 2002EP-00076973.

XX PR 04-JUL-2002; 2002EP-0007674.

XX PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX PI Inze DG, Goossens A, Oksman-Caldentey K, Haekkinen ST, Laakso IU;

XX DR WPI; 2004-022853/02.

XX PT New isolated polypeptides and polynucleotides useful for modulating the

XX PT biosynthesis of secondary metabolites (e.g. alkaloids or

XX PT phenylpropanoids) in an organism or its cell.

PS Claim 2; SEQ ID NO 872; 140pp; English.

XX The present invention describes an isolated polypeptide that modulates  
CC the production of at least one secondary metabolite in an organism, or  
CC its derived cell. The polypeptide is selected from a polypeptide encoded  
CC by a polynucleotide comprising any of the 871 nucleotide sequences given  
CC in the specification. The polypeptides and polynucleotides are useful in  
CC modulating the biosynthesis of secondary metabolites (e.g. alkaloids or  
CC phenylpropanoids) in an organism or its derived cell. The present  
CC sequence is used in the exemplification of the present invention.

SQ Sequence 227 AA;

Query Match 37.8%; Score 400; DB 8; Length 227;  
Best Local Similarity 44.1%; Pred. No. 1e-34;  
Matches 93; Conservative 32; Mismatches 56; Indels 30; Gaps 6;

QY 7 SVSDRFLSLIEEHLSDNSDSSSELTSTEENWEIEFADFLNWS--GSEIQKGS-PS 62  
DB 9 SFSELDPLQSIENHLNLYDSD-----FSSEIFSPMSSSNALPMSPESSFGSPS 56  
QY 63 SESCQSNMASESCQEDSVGTPEPA-----AAGGCGSKDMNRKGVRRRPMWGF 111  
DB 57 AENSILDTSLMDENPEETIQNLSEKSSSEETKGVVAREKNATQWRRTYIGVRRPMWGF 116  
QY 112 AAERIDPKKGRIRWLGTYETPEPDAALAYDAAAFNMRGAKARLNFPHLIGSNISGPRVNP 171  
DB 117 SAERIDPKKGRIRWLGTYETPEPDAALAYDQAAFKIRGRARLNFPHLIGSNIPKPARV 176  
QY 172 PRRKPPAPETSTSSSSSSSSSSSGRKKRR 202  
DB 177 ARSRTRSPQ-PSSSCTSSSEN--GTRKK 204

RESULT 3

AA97227

ID AA97227 standard; protein; 210 AA.

XX AC AA97227;

XX DT 19-DEC-2000 (first entry)

XX DE Plant transcription factor AP2 DNA-binding domain polypeptide.

XX KW AP2; transcription factor; plant metabolism; metabolite; primary;

XX KM secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;

XX KM food colouring; flavouring; fragrance; antimicrobial; pathogenic;

XX KM insecticide; gene expression; modulation.

XX OS Catharanthus roseus.

XX PN WO200046383-A2.

XX PD 10-AUG-2000.

XX PF 07-FEB-2000; 2000WO-NL000075.

XX PR 05-FEB-1999; 99DK-00000158.

XX PR 10-FEB-1999; 99US-0119388P.

XX PA (UYLE-) RIJKSUNIV LEIDEN.

XX PI Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW;

XX DR WPI; 2000-499380/44.

XX DR N-PSDB; AAA53744.

XX PT Modulating level of metabolites and stress resistance in recombinant

XX PT cells for synthesis of plant metabolites such as alkaloids including

XX PT terpenoid indole alkaloids, by providing transcription factor to the

XX PT cell.

XX PS Disclosure, Page 97, 101pp; English.





[illegible]

PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130044P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
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PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
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PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
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PR 28-MAY-1999; 99US-0136782P.  
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PR 08-JUN-1999; 99US-0138094P.  
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PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139458P.  
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PR 09-JUL-1999; 99US-0142920P.  
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PR 19-JUL-1999; 99US-0144331P.  
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PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157532P.  
PR 06-OCT-1999; 99US-0157655P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158639P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.



XX 09-AUG-2001; 2001US-0310847P.  
PR 19-NOV-2001; 2001US-0336049P.  
PR 11-DEC-2001; 2001US-0338692P.  
PR 14-JUN-2002; 2002US-00171468.  
XX  
PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.  
PI Reuber TL, Riechmann JL, Heard JE, Jiang C, Adam LJ, Dubell AN,  
PI Ratcliffe O, Pineda O, Yu GL, Brown PE,  
DR WPI; 2003-256576/25.  
DR N-PSDB; ADE37188.  
XX  
PT New stress-related transcription factor polynucleotides and polypeptides,  
PT useful for producing transgenic plants with e.g. improved tolerance to  
PT diseases or pests, decreased herbicide sensitivity, or improved nutrient  
PT uptake.  
XX  
PS Disclosure; SEQ ID NO 128; 470pp; English.  
XX  
CC The invention relates to a number of cDNA sequence and their encoded  
CC proteins which are especially transcription factor cDNAs and their  
CC proteins. The isolated or recombinant polynucleotide is useful for  
CC producing a modified plant with a modified trait, e.g. enhanced tolerance  
CC to environmental conditions, improved tolerance to microbial, fungal or  
CC viral diseases, improved tolerance to pest infestation, decreased  
CC herbicide sensitivity, improved tolerance to heavy metals, or enhanced  
CC ability to take up heavy metals, improved growth under poor  
CC photoconditions, improved nutrient uptake, or reduced hormone  
CC sensitivity. The transgenic plants are useful for growing a progeny plant  
CC comprising the desired trait. The polynucleotides and polypeptides are  
CC also useful in bioinformatic search methods. This sequence represents one  
CC of the proteins of the invention.  
XX  
SQ Sequence 226 AA;  
XX  
Query Match 33.7%; Score 356.5; DB 7; Length 226;  
Best Local Similarity 61.1%; Pred. No. 5.5e-30;  
Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;  
QY 84 PPEAAGGGS--KDMNRKGVRRRPMGKFAEIRDPKKGSRIMLTGTYETPEDAALAYD 141  
Db 74 PPRTKSGSHAPRGKMGYRGVRRRPMGKFAEIRDPKKGARVWLGTETPEDAALAYD 133  
QY 142 AAAPNMGAKARLNPFLIGSNISGPRVNPRRKFPAPETSSSSSSSEN 194  
Db 134 RAAFOLRGSKAKLNPFLIGSCYKEPVRIRPRRSP-EPSPVQLTSEQRRES 185  
RESULT 12  
AD141543  
ID AD141543 standard; protein; 226 AA.  
XX  
AC AD141543;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Plant transcription factor #3.  
XX  
KM transgenic; plant; enhanced tolerance to abiotic stress;  
KM glycosphate tolerance; hormone sensitivity; disease resistance;  
KM sugar sensing; flowering; flower structure; stem bifurcation;  
KM branching pattern; apical dominance; trichome; stem morphology;  
KM root growth; root hair; seed development; cell proliferation;  
KM cell differentiation; premature senescence; necrosis; plant size;  
KM leaf morphology; seed morphology; seed biochemistry; root anthocyanin;  
KM leaf anthocyanin; light response; shade avoidance; bioinformatic;  
KM transcription factor.  
XX  
OS Arabidopsis thaliana.  
XX  
PN US2004019927-A1.

XX 29-JAN-2004.  
PD  
XX 25-FEB-2003; 2003US-00374780.  
PF  
XX 18-APR-2001; 2001US-00837944.  
PR  
XX (SHER) SHERMAN B K.  
PA (RIEC) RIECHMANN J L.  
PA (JIAN) JIANG C.  
PA (HEAR) HEARD J E.  
PA (HAAR) HAAKE V.  
PA (CREE) CREELMAN R A.  
PA (RATC) RATCLIFFE O.  
PA (ADAM) ADAM L J.  
PA (REUB) REUBER T L.  
PA (KEDD) KEDDIE J.  
PA (BROU) BROUN P E.  
PA (PILG) PILGRIM M L.  
PA (DUBE) DUBELL A N.  
PA (PINE) PINEDA O.  
PA (YUGG) YU G.  
XX  
XX Sherman BK, Riechmann JL, Jiang C, Heard JE, HaaKE V;  
PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE;  
PI Pilgrim ML, Dubell AN, Pineda O, Yu G;  
DR WPI; 2004-132245/13.  
DR N-PSDB; AD141542.  
XX  
PT New transgenic plant comprising a recombinant polynucleotide of any one  
PT of more than 500 nucleotide sequences, useful in bioinformatic search  
PT methods.  
XX  
PS Claim 1; SEQ ID NO 6; 435pp; English.  
XX  
CC The invention describes a transgenic plant comprising a recombinant  
CC polynucleotide of any one of more than 500 nucleotide sequences fully  
CC defined in the specification or its complement. The method of the  
CC invention can be used to produce a plant having altered traits such as:  
CC enhanced tolerance to abiotic stress; glycosphate tolerance; hormone  
CC sensitivity; disease resistance; sugar sensing; early or late flowering;  
CC altered flower structure; change in stem bifurcations; altered branching  
CC pattern; reduced apical dominance; reduced trichome density; lack of  
CC trichomes; reduced ectopic trichome development; altered trichome  
CC development; increase in trichome number; altered stem morphology;  
CC increased root growth; increased root hairs; altered seed development;  
CC altered cell proliferation or cell differentiation; rapid development;  
CC premature senescence; increased necrosis; increase in seedling or plant  
CC size; decreased plant size; leaf morphology; seed morphology; seed  
CC biochemistry; increase in root anthocyanins; increase in plant  
CC anthocyanins; or alteration in light response or shade avoidance. The  
CC transgenic plant, polynucleotides and polypeptides are useful in  
CC bioinformatic search methods. This is the amino acid sequence of a plant  
CC transcription factor that can be used in the creation of a transgenic  
CC plant with altered traits.  
XX  
SQ Sequence 226 AA;  
XX  
Query Match 33.7%; Score 356.5; DB 8; Length 226;  
Best Local Similarity 61.1%; Pred. No. 5.5e-30;  
Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;  
QY 84 PPEAAGGGS--KDMNRKGVRRRPMGKFAEIRDPKKGSRIMLTGTYETPEDAALAYD 141  
Db 74 PPRTKSGSHAPRGKMGYRGVRRRPMGKFAEIRDPKKGARVWLGTETPEDAALAYD 133  
QY 142 AAAPNMGAKARLNPFLIGSNISGPRVNPRRKFPAPETSSSSSSSEN 194  
Db 134 RAAFOLRGSKAKLNPFLIGSCYKEPVRIRPRRSP-EPSPVQLTSEQRRES 185  
RESULT 13

AD001615  
ID AD001615 standard; protein; 226 AA.  
XX  
AC AD001615;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Thalecress transcription factor protein #14.  
XX  
KW Thalecress; transcription factor; plant; transgenic; abiotic stress;  
KW cold tolerance; heat tolerance; drought; osmotic stress;  
KW phosphate limitation; disease resistance; sugar sensing; seed germination;  
KW hormone sensitivity; potassium limitation; nitrogen limitation;  
KW flowering; inflorescence architectural change;  
KW meristem cell differentiation; phylloclax; apical dominance;  
KW trichome development; seed development; premature senescence;  
KW delayed senescence; lethality; necrosis; plant size; leaf morphology;  
KW seed morphology; secondary metabolism; light response; shade avoidance.  
XX  
OS Arabidopsis thaliana.  
XX  
PN US2004045049-A1.  
XX  
PD 04-MAR-2004.  
XX  
PF 10-APR-2003; 2003US-00412699.  
XX  
PR 13-SEP-1999; 99US-00394519.  
PR 21-JAN-2000; 2000US-00489376.  
PR 17-FEB-2000; 2000US-00506720.  
PR 22-MAR-2000; 2000US-00532591.  
PR 22-MAR-2000; 2000US-00533029.  
PR 22-MAR-2000; 2000US-00533030.  
PR 22-MAR-2000; 2000US-00533392.  
PR 22-MAR-2000; 2000US-00533648.  
PR 06-APR-2000; 2000WC-US009448.  
PR 16-NOV-2000; 2000US-00713994.  
PR 27-MAR-2001; 2001US-00819142.  
PR 17-APR-2001; 2001US-00837444.  
PR 30-JAN-2002; 2002US-00958131.  
PR 14-JUN-2002; 2002US-00171468.  
PR 09-AUG-2002; 2002US-00225066.  
PR 09-AUG-2002; 2002US-00225067.  
PR 09-AUG-2002; 2002US-00225068.  
PR 17-DEC-2002; 2002US-0434166P.  
PR 25-FEB-2003; 2003US-00374780.  
XX  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.  
PA (HEAR/) HEARD J E.  
PA (RIEC/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIANG/) JIANG C.  
PA (SAMA/) SAMAH R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
XX  
PI Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE,  
PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS,  
PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R,  
PI Sherman BK;  
XX WPI, 2004-225755/21.  
DR N-PSDB; AD001614.

XX  
PT New transgenic plant, useful in developing phenotypes with altered or  
PT improved characteristics or traits.  
XX  
PS Claim 1; SEQ ID NO 28; 213pp; English.  
XX  
CC The invention relates to a transgenic plant comprising a recombinant  
CC polynucleotide having a polynucleotide sequence or its complementary  
CC sequence comprising a sequence encoding a polypeptide, that initiates  
CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,  
CC Rice, Rape or Corn, comprising any of the sequences appearing as AD001588  
CC AD003527 or AD003530-AD003553. Also included are using a transgenic  
CC plant to grow a progeny plant, an expression cassette (comprising a  
CC constitutive, inducible or tissue-specific promoter and a recombinant  
CC polynucleotide described above), a host cell comprising the expression  
CC cassette, producing a modified plant having a modified trait, identifying  
CC a factor that is modulated by or interacts with a polypeptide encoded by  
CC the polynucleotide sequence and identifying at least one downstream  
CC polynucleotide sequence that is subject to a regulatory effect of any of  
CC the polypeptides encoded by the polynucleotide described above. The  
CC transgenic plant is useful for producing a plant that has an altered  
CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance  
CC to chilling, germination in cold conditions, freezing tolerance, tolerance  
CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to  
CC salt, tolerance to phosphate limitation, tolerance to potassium  
CC limitation, decreased sensitivity to nitrogen limitation), altered  
CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered  
CC response to ethylene, disease resistance, altered susceptibility to  
CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to  
CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered  
CC susceptibility to Sclerotinia, altered sugar sensing, improved seed  
CC germination and seedling vigor, early flowering, late flowering, extended  
CC period of flowering, an inflorescence architectural change, a change in  
CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell  
CC differentiation, altered phylloclax, altered branching pattern, reduced  
CC apical dominance, reduced trichome density, ectopic trichome development,  
CC altered trichome development, altered stem morphology, increased root  
CC growth, increased root hairs, altered seed development, altered cell  
CC proliferation/cell differentiation, premature senescence, delayed  
CC senescence, lethality, increased necrosis, an increase in seedling or  
CC plant size, decreased plant size, a change in leaf morphology, increased  
CC altered leaf development, increased leaf size and mass, glossy leaves,  
CC leaf cell expansion, change in seed morphology, altered seed coloration,  
CC increased seed size, decreased seed size, altered seed shape, change in  
CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid  
CC content, increased leaf insoluble sugars, decreased leaf insoluble  
CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid  
CC content, an alteration of leaf glucosinolate content, change in seed  
CC biochemistry, an increase in seed oil content, decrease in seed oil  
CC content, increase in seed fatty acid content, decrease in seed fatty acid  
CC content, increase in seed protein content, decrease in seed protein  
CC content, alteration in seed prenyl lipid content, increase in seed  
CC sterols, upregulation of genes involved in secondary metabolism, increase  
CC in root anthocyanins, increase in plant anthocyanins, and alteration in  
CC light response or shade avoidance. The present sequence represents a  
CC thalecress transcription factor of the invention.  
XX  
SQ Sequence 226 AA:  
XX  
Query Match 33.7%; Score 356.5; DB 8; Length 226;  
Beat Local Similarity 61.1%; Pred. No. 5.5e-30;  
Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;  
Cy 84 PPEAAAGGCGS--KDMNRYGVRRRPMGKFAAIRDPPKKGSIWIGTYETPDALAYD 141  
Db 74 PPATKASGSHAPROKMGVRRGVRRAAIRDPPKKNGAIVWIGTYETPDAAVAYD 133  
Cy 142 AAAFNMGAKARLNFPHLIGSNISGPRVVRPRKFAEPSTSSSSSSSEN 194  
Db 134 RAAFGRLGSKAKNFPHLIGSKYEPVRIRPRRSP-FPSVDSQULTSQRRES 185  
RESULT 14



Tue Mar 8 08:51:48 2005

us-09-890-782-6.rag

Page 16

Job time : 165 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 27, 2005, 21:57.33 ; Search time 40 Seconds

(without alignments)  
488.300 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 1058  
Sequence: 1 MBEIISVDRFLSLIEH.....SSSSSSSSSENSGKRRY 203

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 28346 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 28346

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

1: d1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	356.5	33.7	226	T00409	ethylene-responsive
2	353	33.4	226	T02432	ethylene-responsive
3	338	31.9	243	T51989	ethylene-responsive
4	333	31.5	233	T02590	DNA binding protei
5	328.5	31.0	234	T07686	transcription fact
6	322	30.4	266	T51988	ethylene responsiv
7	312	29.5	225	A85196	EREBP-2 protein [1
8	286.5	27.1	244	B86197	hypotheical prote
9	282.5	26.7	207	T49897	transcription fact
10	266	25.1	161	T07680	transcription fact
11	265.5	25.1	268	T04787	hypotheical prote
12	263	24.9	133	D86175	hypotheical prote
13	263	24.9	218	F84748	probable AP2 domai
14	262.5	24.8	291	T02434	DNA binding protei
15	257.5	24.3	236	B84718	hypotheical prote
16	253	23.9	204	S49031	cadmium-induced pr
17	249.5	23.6	225	T52011	ethylene responsiv
18	248.5	23.5	358	D96579	hypotheical prote
19	245	23.2	603	B71444	probable EREBP-4 -
20	244.5	23.1	212	T48540	hypotheical prote
21	244	23.1	236	T48518	transcription fact
22	241.5	22.8	277	T03927	DNA binding protei
23	241	22.8	300	T52020	ethylene responsiv
24	240.5	22.7	281	T52189	ethylene responsiv
25	240	22.7	314	B86482	protein F5U5.5 [im
26	239.5	22.6	176	T00498	probable AP2 domai
27	237	22.4	259	T52619	TINY-like protei
28	234.5	22.2	204	B86410	protein F3M18.20 [
29	232.5	22.0	218	T01076	transcription fact

30	232.5	22.0	295	2	T00399	probable AP2 domai
31	232	21.9	171	2	T00432	probable AP2 domai
32	232	21.9	196	2	G85435	TINY-like protei
33	232	21.9	263	2	T49870	probable transcrip
34	231.5	21.9	192	2	D96498	RA2.6 (imported)
35	230.5	21.8	225	2	T02433	DNA binding protei
36	230	21.7	303	2	T04541	hypotheical prote
37	229.5	21.7	262	2	E96747	hypotheical prote
38	227.5	21.5	185	2	D96572	protein F12M16.6 [
39	225.5	21.3	222	2	T52019	ethylene responsiv
40	224	21.2	245	2	B86168	hypotheical prote
41	224	21.2	336	2	B84594	AP2 domain transcr
42	223	21.1	251	2	T01986	Ts11 protein - com
43	222.5	21.0	328	2	G86263	hypotheical prote
44	222	21.0	328	2	G84826	hypotheical prote
45	220	20.8	343	2	T05607	hypotheical prote

#### ALIGNMENTS

RESULT 1  
T00409  
ethylene-responsive transcription factor homolog T13E15.15 - Arabidopsis thaliana  
N:Alternate names: hypotheical protein At2g44840  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004  
R:Accession: T00409; D84883  
R:Roundley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mas  
submitted to the EMBL Data Library, July 1997  
A:Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.  
A:Reference number: Z14146  
A:Accession: T00409  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-226 <ROU>  
A:Cross-references: UNIPROT:Q02167; EMBL:AC002388; NID:G3420042; PID:G2344900  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.  
euse, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MID:20083487; PMID:10617197  
A:Accession: D84883  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-226 <STO>  
A:Cross-references: GB:AE002093; NID:G2344900; PIDN:AAC31840.1; GSPDB:GN00139  
C:Genetic:  
A:Gene: At2g44840; T13E15.15  
A:Map position: 2

Query Match 33.7%; Score 356.5; DB 2; Length 226;  
Best Local Similarity 61.1%; Pred. No. 9 6e-24;  
Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;

QY 84 PPEAAGGGS-KDMNRYGVRRPQKFAEIRDPKKGSRIMVGTETPEDAALAYD 141  
DB 74 PPAATKASGSHAPQKMGQYRGVRRPQKFAEIRDPKKGARVIMVGTETPEDAAYD 133  
QY 142 AAATFNRGAKARINPFLIGSNISGVYVNRKRFPAEISTSSSSSSSEN 194  
DB 134 RAATFNRGAKARINPFLIGSNISGVYVNRKRFPAEISTSSSSSSSEN 185

RESULT 2  
T02432  
ethylene-responsive transcription factor ERF1 - common tobacco  
C:Species: Nicotiana tabacum (common tobacco)  
C>Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T02432  
R:Ohme-Takagi, M.; Shinshi, H.



Plant Cell 7, 173-182, 1995  
A/Title: Ethylene-inducible DNA binding proteins that interact with an ethylene response  
A/Reference number: Z14671, MUID:95276459, PMID:7756828  
A/Accession: T02432  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-236 <OHM>  
A/Cross-references: UNIPROT:Q0476; EMBL:D38123; NID:g790359; PIDN:BAA07321.1; PID:g1208  
A/Experimental source: strain BY4, tissue-type leaf

Query Match 33.4%; Score 353; DB 2; Length 236;  
Best Local Similarity 45.3%; Pred. No. 2e-23;  
Matches 81; Conservative 20; Mismatches 50; Indels 28; Gaps 6;

QY 27 DSSSLSTSTSEEWEIFADPLN--WSGEIQRKSPSSSCQNSMAESCQEDSVGTP 84  
DB 46 DSEEDMVIYT-----LKDALNVGKSPNF--SAGEVNSEQ-----REETIVSP 88  
QY 85 PEAAGGCGSKDMNR-YKGVRRRPMGKFAAEIRDPKKGSRITWLTGYETTPEDALAYDAA 143  
DB 89 AETTAAPAAELPRGRHYRGVRRPMGKFAAEIRDPKKGARVWLTGYETDEBAALAYDKA 148  
QY 144 APMRGAKARLNPPLHIGNISGPVAVNPKRFPAPSPSTSSSSSSSSSSSGGKRRK 202  
DB 149 AYMRGSKALNPPHRIGLNEPEPVATKRRASPEP-----ASSSSNSPKRRK 199

## RESULT 3

T51989  
ethylene responsive element binding factor 2 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C/Accession: T51989  
R:Fujimoto, S.Y.; Ohta, M.; Usui, A.; Shinshi, H.; Ohme-Takagi, M.  
Plant Cell 12, 393-404, 2000  
A/Title: Arabidopsis ethylene responsive element binding factors act as transcriptional  
A/Reference number: Z25893  
A/Accession: T51989  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-243 <FUY>  
A/Cross-references: UNIPROT:O80338; EMBL:AB008104; PIDN:BAA32419.1  
A/Genetic: A:Gene: ERF-2

Query Match 31.9%; Score 338; DB 2; Length 243;  
Best Local Similarity 39.4%; Pred. No. 4.3e-22;  
Matches 85; Conservative 30; Mismatches 69; Indels 32; Gaps 6;

QY 9 SDRFLSLIEHLLSNDSSSELTSTENNBEIFADPLNMSGSEIQRKGS----- 60  
DB 9 SDVALLSEITRHLGGGCGE---NELRANSTSPSCCTE--SWGCLPKENDEMDLVYGL 63  
QY 61 -PSSSCQNSMAESCQED-----SVGTPEAAAGGCGSKDMNRKYGVRR 106  
DB 64 LKDAFFHFDSSSDLSCLFDPFAVKVPTENFTAMEBKPKKAIPTETAVKAGHYGVRR 123  
QY 107 PMGKFAAEIRDPKKGSRITWLTGYETTPEDALAYDAAAPMGAKARLNPPLHIGNISG 166  
DB 124 PMGKFAAEIRDPKKGARVWLTGYETDEBAALAYDAAAPMGKSRALNPPHRIGLNEPEP 183  
QY 167 PVAVNPKRFPAPSPSTSSSSSSSSSSSGGKRRK 202  
DB 184 PVAVNPKRFPAPSPSTSSSSSSSSSSSGGKRRK 214

RESULT 4  
T02590  
DNA binding protein ERBP-2 - common tobacco  
C/Species: Nicotiana tabacum (common tobacco)  
C/Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C/Accession: T02590  
R:Ohme-Takagi, M.; Shinshi, H.

Plant Cell 7, 173-182, 1995  
A/Title: Ethylene-inducible DNA binding proteins that interact with an ethylene response  
A/Reference number: Z14671, MUID:95276459, PMID:7756828  
A/Accession: T02590  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-233 <OHM>  
A/Cross-references: UNIPROT:Q0479; EMBL:D38126; NID:g790362; PIDN:BAA07324.1; PID:g1208  
A/Experimental source: strain BY4, tissue-type leaf

Query Match 31.5%; Score 333; DB 2; Length 233;  
Best Local Similarity 54.9%; Pred. No. 1.1e-21;  
Matches 67; Conservative 16; Mismatches 35; Indels 4; Gaps 2;

QY 81 VGTPEAAAGCGSKDMNRKYGVRRRPMGKFAAEIRDPKKGSRITWLTGYETTPEDALAY 140  
DB 80 VAPPAETTAQAVVPKGRHYRGVRRPMGKFAAEIRDPKKGARVWLTGYETDEBAALAY 139  
QY 141 DAAAFNRGAKARLNPPLHIGNISGPVAVNPKRFPAPSPSTSSSSSSSSSGGKRRK 200  
DB 140 DKAAVMRGSKALNPPHRIGLNEPEPVATKRRSP-EP--ASSISSALENGSPKRR 195  
QY 201 RR 202  
DB 196 RK 197

## RESULT 5

T07686  
transcription factor Pti4 - tomato (fragment)  
C/Species: Lycopersicon esculentum (tomato)  
C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C/Accession: T07686  
R:Zhou, J.; Tang, X.; Martin, G.B.  
submitted to the EMBL Data Library, July 1998  
A/Reference number: Z16094  
A/Accession: T07686  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-234 <ZHO>  
A/Cross-references: UNIPROT:Q04680; EMBL:U89255; NID:g3342210; PIDN:AAC50047.1; PID:g334  
A/Function: A:Description: transcription factor  
A/Note: binds the GCC box, present in the promoter region of genes encoding pathogenesis  
C/Keywords: DNA binding; transcription factor

Query Match 31.0%; Score 328.5; DB 2; Length 234;  
Best Local Similarity 47.1%; Pred. No. 2.8e-21;  
Matches 73; Conservative 18; Mismatches 43; Indels 21; Gaps 5;

QY 49 NMSGSEIQRKSPSSSCQNSMAESCQEDSVGTPPEAAAGGCGSKDMNR-YKGVRRRP 107  
DB 65 NFTAGEV--KSEPRRE-----TESSPERS--PSAETTTAAPAATPKGRHYRGVRRP 113  
QY 108 WGFPAEIRDPKKGSRITWLTGYETTPEDALAYDAAAFNRGAKARLNPPLHIGNISG 167  
DB 114 WGFPAEIRDPKKGARVWLTGYETDEBAALAYDKAAVMRGSKALNPPHRIGLNEPEP 173  
QY 168 VRVAVNPKRFPAPSPSTSSSSSSSSSSSGGKRRK 202  
DB 174 VRVAVNPKRFPAPSPSTSSSSSSSSSSSGGKRRK 199

## RESULT 6

T51988  
ethylene responsive element binding factor 1 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 20-Oct-2000  
C/Accession: T51988  
R:Fujimoto, S.Y.; Ohta, M.; Usui, A.; Shinshi, H.; Ohme-Takagi, M.  
Plant Cell 12, 393-404, 2000  
A/Title: Arabidopsis ethylene responsive element binding factors act as transcriptional  
A/Reference number: Z25893



Qy 11 AAEIRPDKKGGSSITWGTETEPEDALAYDAADAFMNGAKRLNPHLIGNSISGPV--- 168  
Db 122 AAEIRPDKKGGSSITWGTETEPEDDAARANDCAAFRLRKRKVLNFP-LDAGKYEAPANGS 180  
Qy 169 RVNPRKRPPEAPETSTSSSSSSSSSE 193  
Db 181 RKRKSDVHELORTQSSSSSSSSCD 205

RESULT 10

C:transcription factor Ptl5 - tomato  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C:Accession: 107689  
R:Zhou, J.; Tang, X.; Martin, G.B.  
EMBO J. 16, 3207-3218, 1997  
A:Title: The Pto kinase conferring resistance to tomato bacterial speck disease interact  
A:Reference number: Z16096; MUID:97357308; PMID:9214637  
A:Accession: 107689  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-161 <ZHO>  
A:Cross-references: UNIPROT:O04681; EMBL:U89256; NID:g2213782; PIDN:AAC49740.1; PID:g221  
C:Function:  
A:Description: transcription factor  
A:Note: binds the GCC box, present in the promoter region of genes encoding pathogenesis  
:Keywords: DNA binding; transcription factor

Query Match	25.1%	Score 266;	DB 2;	Length 161;
Best Local Similarity	55.6%	Pred. No. 4.9e-16;		
Matches	55;	Conservative	17;	Mismatches 23;
			Indels	4;
			Gaps	2

```
OY      99 RYKGYRRRPBGKFAAEIRDPKKKGSIWLGTIETBEDAALAYDAAAFNRMGAKARLNPPH 158  
       ::::|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
Db     58 KYRGYRRRPRPGKYAAEIRDSARHGAVWLGTPETAEEAALAYDRAAFNRMGAKALNPPS 117
```

Oy 159 LIGNSICGVRVNPCKFPAPBPTTSSSSSSSSSSSSG 197  
 Db 118 EI---VNASVSV-D-KLSLCSNSTYTTNNNSDSSLNEVSSG 152

## RESULT 11

hypothetical protein F10M10.180 - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C/Accession: T04787  
R/Beran, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hohnleis, J.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999  
A/Reference number: Z15384  
A/Accession: T04787  
A/Molecule type: DNA  
A/Residues: 1-268 <BEV>  
A/Cross-references: UNIPROT:Q9SC06; EMBL:AL035521  
A/Experimental source: cultivar Columbia; BAC clone F10M10  
C/Genetics:  
A/Map position: 4  
A/Note: F10M10.180

Query Match	25.1%;	Score 265.5;	DB 2;	Length 268;
Best Local Similarity	37.8%;	Pred. No. 1e-15;		
Matches 70;	Conservative 25;	Mismatches 47;	Indels 43;	Gaps 9

```

Oy 51 SGEIQRGSRP--SSSSCSNSMAEC-----QESVYGT-----83
      |||::|
Db 55 SbstVtSAGPRHLDSTQCV-CRIECLGcNFPAPnQRIENQOBEIITSSNRRES 113
      |||::|

Oy 84 ----PPEAAGGCGSxDMNR---YKQYRRPRPMGKFAAEIRDPKKKGSRIWLTGYTPEDAA 137
      |||::|
Db 114 SPVAKKAEAGGGKTRKRKNKKNGRGVRQKPFMGKFAAEIRDP--KRTIRWALGTFTETADAA 172
      |||::|

```

```
QY      138  LAVDAAAFNNRGAKARLNFPHL-IGSNISGPVRVPRKRPAAEPSTSSSSSSSSSE---193
      173  RAIDRAALIGRGRALTNFPFVDYTSVSSSPVAAD---IGAKSASASVSATDSVEAEQ 229
QY      194  -NSGG 197
Db      230  WNGGG 234
```

RESULT 12

hypothetical protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
A:Accession: D86175  
R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,  
ansen, N.F.; Hughes, B.; Hutzar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzall,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salbeck, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: D86175  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-133 <STO>  
A:Cross-references: UNIPROT:P93822; GB:AE005172; NID:g1903356; PIDD:AA070439.1; GSPDB:GN  
C:Genetics:  
A:Map position: 1

Query Match	24.9%;	Score 263;	DB 2;	Length 133;
Best Local Similarity	47.7%;	Pred. No. 7.1e-16;		
Matches	51;	Conservative	17;	Mismatches 25;
			Indels	14;
			Gaps	1

```
Oy      87 AAAGGGCKWMNRYGVRRPWWGKFAAEIRDPKKSKSRIMWTGTETPEDALAYDAAAFN 146
```

:: :: :::::::::::::::::::: : ::::: | ||| :::

```
Ddb     7 SSGSggGAQGKYRGVRRRPWGKFAAERDRKHGERVMWLTGFDTMEDDAARAYDRAYS 66
```

```
Oy      147 MRGAKARLNFPHLIGSNISGPVRVNPKRKPEAPESTSSSSSSSSSE 19
          ||| ||||| |:::||||| :
Db      67 MRGKAALNFPHEYMGTS-----SSTAANSSSSSQ 99
```

## RESULT 13

Probable AP2 domain transcription factor [Imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: F84748  
 R:Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentol, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
 Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: AB4420; MUID:20083487; PMID:10617197  
 A:Accession: F84748  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-218 <STO>  
 A:Cross-references: UNIPROT: P93007; GB:AE002093; NID:91707016; PIDN: AAC69127.1; GSPDB:GN  
 C:Genetics:  
 A:Gene: At2g33710  
 A:Map position: 2

Query March 24.9%; Score 263; DB 2; Length 218;  
 Beest local Similarity 41.0%; Pred. No. 1.3e-15;  
 Matches 64; Conservative 24; Mismatches 38; Indels 30; Gaps 6

28 DSSSELTSTEENWEEIFADFLNWSGSEIQKRGSPSSSESCQSNMAESCQEDSVGTPEA 87



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 27, 2005, 22:06:15 ; Search time:130 Seconds

(without alignments)  
512.254 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 1058  
Sequence: 1 MSEELISVDRFLSLIEH.....SSSSSSSSSSSGRKKRRY 203

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 138539 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 138539

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:  
1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubppa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubppa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubppa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	356.5	33.7	226	US-10-225-068-128	Sequence 128, App
2	356.5	33.7	226	US-10-374-780A-6	Sequence 6, Appl1
3	356.5	33.6	226	US-10-412-699B-28	Sequence 28, Appl1
4	356	33.7	202	US-10-424-599-175489	Sequence 175489,
5	345	32.6	282	US-10-374-780A-503	Sequence 503, App
6	338	31.9	243	US-09-533-029-34	Sequence 34, Appl
7	338	31.9	243	US-09-934-455-416	Sequence 416, App
8	338	31.9	243	US-10-374-780A-2074	Sequence 2074, Ap
9	338	31.9	243	US-10-412-699B-670	Sequence 670, App
10	338	31.9	243	US-10-412-699B-1832	Sequence 1832, Ap
11	338	31.9	248	US-10-425-114-41687	Sequence 41687, A
12	331.5	31.3	156	US-10-424-599-208822	Sequence 208822,
13	330.5	31.2	311	US-10-425-114-43402	Sequence 43402, A

14	324	30.6	268	10	US-09-533-029-18	Sequence 18, Appl
15	324	30.6	268	10	US-09-934-455-2	Sequence 2, Appl1
16	324	30.6	268	15	US-10-225-068-196	Sequence 196, App
17	324	30.6	268	15	US-10-374-780A-10	Sequence 10, Appl
18	324	30.6	268	15	US-10-412-699B-38	Sequence 38, Appl1
19	324	30.6	268	17	US-10-495-918-102	Sequence 102, App
20	322.5	30.5	318	16	US-10-437-963-183672	Sequence 183672,
21	322	30.4	328	16	US-10-437-963-119150	Sequence 121950,
22	316.5	29.9	318	16	US-10-437-963-145941	Sequence 145941,
23	309.5	29.3	147	15	US-10-424-599-242420	Sequence 242420,
24	309.5	29.3	147	15	US-10-424-599-146343	Sequence 146343,
25	306	28.9	240	15	US-10-424-599-220299	Sequence 220299,
26	306	28.9	240	16	US-10-437-963-118008	Sequence 118008,
27	302.5	28.6	199	15	US-10-424-599-214365	Sequence 214365,
28	302.5	28.6	195	15	US-10-425-114-36689	Sequence 36689, A
29	299	28.3	195	15	US-10-424-599-173756	Sequence 173756,
30	299	28.3	211	15	US-10-425-114-56040	Sequence 56040, A
31	298.5	28.2	231	14	US-10-122-822-1	Sequence 1, Appl1
32	297.5	28.1	259	15	US-10-374-780A-501	Sequence 501, App
33	297.5	28.1	229	15	US-10-412-699B-1000	Sequence 1000, Ap
34	294	27.8	271	15	US-10-310-154-476	Sequence 476, App
35	292	27.6	240	15	US-10-425-114-39862	Sequence 39862, A
36	292	27.6	344	16	US-10-437-963-152032	Sequence 152032,
37	286.5	27.1	244	15	US-10-225-068-474	Sequence 474, Appl
38	286.5	27.1	244	15	US-10-225-067-106	Sequence 106, App
39	286.5	27.1	244	15	US-10-374-780A-2876	Sequence 2876, Ap
40	286.5	27.0	201	15	US-10-225-066A-788	Sequence 788, App
41	285.5	27.0	201	15	US-10-374-780A-2230	Sequence 2230, Ap
42	285.5	27.0	201	15	US-10-412-699B-50	Sequence 50, Appl
43	285.5	27.0	201	15	US-10-412-699B-1726	Sequence 1726, Ap
44	285.5	27.0	201	15	US-10-767-701-36377	Sequence 36377, A
45	285	26.9	135	16	US-10-767-701-36377	Sequence 36377, A

#### ALIGNMENTS

RESULT 1  
US-10-225-068-128  
; Sequence 128, Application US/10225068  
; Publication No. US20030217383A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendel Biotechnology, Inc.  
; APPLICANT: Reuber, T. Lynne  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Heard, Jacqueline E.  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Adam, Luc J.  
; APPLICANT: Dubell, Arnold T.  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Plineda, Omaria  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Brown, Pierre E.  
; TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND  
; POLYPEPTIDES IN PLANTS  
; FILE REFERENCE: 514442002040  
; CURRENT APPLICATION NUMBER: US/10/225,068  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 60/310,847  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/336,049  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/338,692  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: 10/171,468  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 128  
; LENGTH: 226  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:

NAME/KEY: DOMAIN  
LOCATION: (89)...(157)  
OTHER INFORMATION: Conserved domain  
US-10-225-068-128

Query Match 33.7%; Score 356.5; DB 15; Length 226;  
Best Local Similarity 61.1%; Pred. No. 7.6e-27;  
Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;

QY 84 PPEAAAGGCS--KDNRRKGVRRPWPCKFAAEIRDPKKKSGRIWLGTYETEDAAAYD 141  
DB 74 PPATKASGSHAPQKMQYRGVRRPWPCKFAAEIRDPKNGARVWLGTYETEDAAVAYD 133  
QY 142 AAAFNMGAKARLNPFLIGSNISGVRVNPRRKRPAPESPSTSSSSSSSEN 194  
DB 134 RAAFQJRGSKAKLNPFLIGSCYEPVRI RPRRSP-EPSPVDQLTSEQKRES 185

## RESULT 2

US-10-374-780A-6  
Sequence 6, Application US/10374780A  
Publication No. US20040019927A1  
GENERAL INFORMATION:  
APPLICANT: Sherman, Bradley K  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Heard, Jacqueline E  
APPLICANT: Haake, Volker  
APPLICANT: Creelman, Robert A  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Adam, Luc J  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddie, James  
APPLICANT: Brown, Pierre E  
APPLICANT: Pilgrim, Marsha L  
APPLICANT: Dubell III, Arnold T  
APPLICANT: Pineda, Omaira  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
FILE REFERENCE: MBI-0047 CIP  
CURRENT APPLICATION NUMBER: US/10/374, 780A  
CURRENT FILING DATE: 2003-02-25  
PRIOR APPLICATION NUMBER: 09/837,944  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/934,455  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
PRIOR APPLICATION NUMBER: 10/225,066  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,067  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,068  
PRIOR FILING DATE: 2002-08-09  
NUMBER OF SEQ ID NOS: 2906  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 6  
LENGTH: 226  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
OTHER INFORMATION: G22 (conserved domain in AA coordinates: 89-157)  
US-10-374-780A-6

Query Match 33.7%; Score 356.5; DB 15; Length 226;  
Best Local Similarity 61.1%; Pred. No. 7.6e-27;  
Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;

QY 84 PPEAAAGGCS--KDNRRKGVRRPWPCKFAAEIRDPKKKSGRIWLGTYETEDAAAYD 141  
DB 74 PPATKASGSHAPQKMQYRGVRRPWPCKFAAEIRDPKNGARVWLGTYETEDAAVAYD 133

QY 142 AAAFNMGAKARLNPFLIGSNISGVRVNPRRKRPAPESPSTSSSSSSSEN 194  
DB 134 RAAFQJRGSKAKLNPFLIGSCYEPVRI RPRRSP-EPSPVDQLTSEQKRES 185

## RESULT 3

US-10-412-699B-28  
Sequence 28, Application US/10412699B  
Publication No. US20040045049A1  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: Zhang, James  
APPLICANT: Fromm, Michael E.  
APPLICANT: Heard, Jacqueline E.  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Adam, Luc J.  
APPLICANT: Brown, Pierre E.  
APPLICANT: Pineda, Omaira  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddie, James S.  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Samaha, Raymond R.  
APPLICANT: Pilgrim, Marsha L.  
APPLICANT: Creelman, Robert A.  
APPLICANT: Dubell, Arnold N.  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Kumimoto, Roderick  
APPLICANT: Sherman, Bradley K  
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants  
FILE REFERENCE: MBI-0048CIP  
CURRENT APPLICATION NUMBER: US/10/412,699B  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: 09/394,519  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: 09/489,376  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: 09/506,720  
PRIOR FILING DATE: 2000-02-17  
PRIOR APPLICATION NUMBER: 09/533,030  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,392  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,029  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/532,591  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,648  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/713,994  
PRIOR FILING DATE: 2000-11-16  
PRIOR APPLICATION NUMBER: 09/819,142  
PRIOR FILING DATE: 2001-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2011  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 28  
LENGTH: 226  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
OTHER INFORMATION: G22  
US-10-412-699B-28

Query Match 33.7%; Score 356.5; DB 15; Length 226;  
Best Local Similarity 61.1%; Pred. No. 7.6e-27;  
Matches 69; Conservative 15; Mismatches 26; Indels 3; Gaps 2;



```

OY      84  PEEAALGGGCS--KOMNRKGVRRPWPWGFPAEIRDPKKKSGSIWGTETPEDAALAYD 141
Db      74  PPATVASSSHAPRQGMQVGRVRRRRWKGFAEIRDPKKNGGARVWLTGYTETPEDAANAYD 133
OY      142 AAAFEMRGAKALNFPHLIGNISGVGVNRPKRFPAEFGTSSSSSSSEN 194
Db      134 RAAPFQSRKALKALNPHLIGSCKEPVRIRPRRSP--EPBVSQULTSEQRRS 185

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RESULT 4  
US-10-424-599-175489  
; Sequence 175489, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J  
 APPLICANT: Kovalic David K  
 APPLICANT: Zhou Yihua  
 APPLICANT: Cao Yongwei  
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 FILE REFERENCE: 38-21(53223)B  
 CURRENT APPLICATION NUMBER: US/10/424,599  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 285684  
 SEQ ID NO 175489  
 LENGTH: 202  
 TYPE: PRT  
 ORGANISM: Glycine max  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT3847\_129485C.1 pep  
 US-10-424-599-175489

Query Match	33.6%	Score 356;	DB 15;	Length 202;
Best Local Similarity	41.3%	Pred. No. 7.4e-27;		
Matches	83;	Conservative	29;	Mismatches 55;
			Indels	34;
			Gaps	5;

[illegible]

RESULT 5  
US-10-974-780A-503  
: Sequence 503, Application US/10374780A  
: Publication No. US20040019927A1  
: GENERAL INFORMATION:  
: APPLICANT: Sherman, Bradley J  
: APPLICANT: Riechmann, Jose Luis  
: APPLICANT: Liang, Cal-Zhong  
: APPLICANT: Heard, Jacqueline E  
: APPLICANT: Haake, Volter  
: APPLICANT: Creelman, Robert A  
: APPLICANT: Ratcliffe, Oliver  
: APPLICANT: Adam, Luc J  
: APPLICANT: Reubert, T. Lynne  
: APPLICANT: Keddie, James  
: APPLICANT: Brown, Pierre E  
: APPLICANT: Pilgrim, Marsha L  
: APPLICANT: Dubell III, Arnold T  
: APPLICANT: Pineda, Omarita  
: APPLICANT: Yu, Guo-Liang

```

1  TITLE OR INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
2  FILE REFERENCE:  MB1-0047 CIP
3  CURRENT APPLICATION NUMBER:  US/10/374,780A
4  PRIOR FILING DATE:  2003-02-25
5  PRIOR APPLICATION NUMBER:  09/837,944
6  PRIOR FILING DATE:  2001-04-18
7  PRIOR APPLICATION NUMBER:  60/310,847
8  PRIOR FILING DATE:  2001-08-09
9  PRIOR APPLICATION NUMBER:  09/934,455
10 PRIOR FILING DATE:  2001-08-22
11 PRIOR APPLICATION NUMBER:  60/336,049
12 PRIOR FILING DATE:  2001-11-19
13 PRIOR APPLICATION NUMBER:  60/338,592
14 PRIOR FILING DATE:  2001-12-11
15 PRIOR APPLICATION NUMBER:  10/111,468
16 PRIOR FILING DATE:  2002-06-14
17 PRIOR APPLICATION NUMBER:  10/225,066
18 PRIOR FILING DATE:  2002-08-09
19 PRIOR APPLICATION NUMBER:  10/225,067
20 PRIOR FILING DATE:  2002-08-09
21 PRIOR APPLICATION NUMBER:  10/225,068
22 PRIOR FILING DATE:  2002-08-09
23 NUMBER OF SEQ ID NOS: 2906
24 SOFTWARE: PatentIn version 3.2
25 SEQ ID NO 503
26 LENGTH: 282
27 TYPE: PRT
28 ORGANISM: Mesembryanthemum crystallinum
29 FEATURE:
30 OTHER INFORMATION: Orthologous to G28
31 US-10-374-780A-503

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Query Match	32.6%	Score 345;	DB 15;	Length 282;
Best Local Similarity	40.5%	Pred. No. 1.4e-25;		
Matches	96;	Conservative	22;	Mismatches 65;
				Indels 56;
				Gaps 10;

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QY      9 SDFLLSLIEHLLSD-----NDDSS-----SELSTEEN 39
      11 : | | | | | | | | | | | | | | | | | | | |
Db      9 SDAVLESIIRHLLIEDMDPRAGAPATTGGSGPVYHRNSSFSLYCLTDNKGELPLEDD 68
      11 : | | | | | | | | | | | | | | | | | | | |
QY      40 WEELF-----ADFLNW-----SGSEIQKRGSPSSHCOSNMAESCQEDSVYCTP--DEAA 88
      11 : | | | | | | | | | | | | | | | | | | | |
Db      69 SEMVLFGYLRDAVHTGMSPOSGE--SGSGSPAPVTVYKEPV-----DSVSSPAVVRV 122
      11 : | | | | | | | | | | | | | | | | | | | |
QY      89 AGC-----CCKSDMRYKGVRRPWPGEAAEIRDPKKGSRITWLTETPEDALAYDAA 144
      11 : | | | | | | | | | | | | | | | | | | | |
Db      122 AGGEAAVAAAAPARGKHYRCVRRRPWGKFAAEIRDPADKAGAVWLGTETBEDAALAYDRA 181
      11 : | | | | | | | | | | | | | | | | | | | |
QY      144 AFNMRGAKARLNFPHLIGSNISGPRVNPGRFPAPETSSSSSSSSSENGGRKK 200
      11 : | | | | | | | | | | | | | | | | | | | |
Db      182 AFMRKSKALLNPLRVNSGEPDPVRIYTKRSP--ERSVSSSSSESSAPRK--RKK 224
      11 : | | | | | | | | | | | | | | | | | | | |

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RESULT 6 0-029-34  
US-09-533-029-34  
Sequence 34, Application US/09533029  
Publication No. US20030046723A1  
GENERAL INFORMATION:  
APPLICANT: Heard, Jacqueline  
APPLICANT: Broun, Pierre  
APPLICANT: Riechmann, Jose-Luis  
APPLICANT: Keddie, James  
APPLICANT: Pineda, Omatra  
APPLICANT: Adam, Luc  
APPLICANT: Samaha, Raymond  
APPLICANT: Zhuo, James  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Pilgrim, Marsha  
APPLICANT: Jhang, Cai-Zhong  
APPLICANT: Reuber, Lynne  
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES  
FILE REFERENCE: MBI-010

;; CURRENT APPLICATION NUMBER: US/09/533,029  
;; CURRENT FILING DATE: 2000-03-22  
;; EARLIER APPLICATION NUMBER: 60/125,814  
;; EARLIER FILING DATE: 1999-03-23  
;; NUMBER OF SEQ ID NOS: 121  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 34  
;; LENGTH: 243  
;; TYPE: PRT  
;; ORGANISM: Arabidopsis thaliana  
;; FEATURE:  
;; OTHER INFORMATION: G1006  
US-09-533-029-34

Query Match 31.9%; Score 338; DB 10; Length 243;  
Best Local Similarity 39.4%; Pred. No. 5.7e-25;  
Matches 85; Conservative 30; Mismatches 69; Indels 32; Gaps 6;

QY 9 SDRFLSLIEHLSDNSDSSSELTSTEENWEIIFADFLNWSGEIQRGS-----60  
DB 9 SDVALLSEITRHLGGGGE---NELRLNSTPSSCTE--SWGGLPKENSEDMLVYGL 63  
QY 61 -PSESCQNSMAESQED-----SVGTPEPAAAGGCGCKDMNRYGVRR 106  
DB 64 LKDAFHFDITSSDLSCLFDPFAVKVEPTENFTAMEKPKKAIPTETAVKAGHYRGVRR 123  
QY 107 PMGKFAAEIRDPKKKSRIWLGTYETPEDAALAYDAAFNMGAKARLNPPLIGSNISG 166  
DB 124 PMGKFAAEIRDPKNGARWLGTFETAEADALAYDAAFRMGRSRLNPLRVNSGEPD 183  
QY 167 PVRVNPKRFPAPFPSTSSSSSSSSSENGGRRKR 202  
DB 184 PVRITSKR---SSSSSSSSSSSTSSSEN--GKLKRR 214

RESULT 7  
US-09-934-455-416  
;; Sequence 416, Application US/09934455  
;; Publication No. US20030121070A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Adam, Luc  
;; APPLICANT: Creelman, Robert  
;; APPLICANT: Dubell, Arnold  
;; APPLICANT: Heard, Jacqueline  
;; APPLICANT: Jiang, Cai-Zhong  
;; APPLICANT: Keddie, James  
;; APPLICANT: Pilgrim, Marsha  
;; APPLICANT: Ratcliffe, Oliver  
;; APPLICANT: Reuber, Lynne  
;; APPLICANT: Riechmann, Jose Luis  
;; APPLICANT: Yu, Guo-Liang  
;; APPLICANT: Pineda, Omaira  
;; TITLE OF INVENTION: Genes for Modifying Plant Traits IV  
;; FILE REFERENCE: MBI-0025  
;; CURRENT APPLICATION NUMBER: US/09/934,455  
;; CURRENT FILING DATE: 2001-08-22  
;; PRIOR APPLICATION NUMBER: 60/227439  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: MBI-0022  
;; PRIOR FILING DATE: 2001-11-16  
;; PRIOR APPLICATION NUMBER: MBI-0023  
;; PRIOR FILING DATE: 2001-04-17  
;; NUMBER OF SEQ ID NOS: 516  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 416  
;; LENGTH: 243  
;; TYPE: PRT  
;; ORGANISM: Arabidopsis thaliana  
US-09-934-455-416

Query Match 31.9%; Score 338; DB 10; Length 243;  
Best Local Similarity 39.4%; Pred. No. 5.7e-25;  
Matches 85; Conservative 30; Mismatches 69; Indels 32; Gaps 6;

QY 9 SDRFLSLIEHLSDNSDSSSELTSTEENWEIIFADFLNWSGEIQRGS-----60  
DB 9 SDVALLSEITRHLGGGGE---NELRLNSTPSSCTE--SWGGLPKENSEDMLVYGL 63  
QY 61 -PSESCQNSMAESQED-----SVGTPEPAAAGGCGCKDMNRYGVRR 106  
DB 64 LKDAFHFDITSSDLSCLFDPFAVKVEPTENFTAMEKPKKAIPTETAVKAGHYRGVRR 123  
QY 107 PMGKFAAEIRDPKKKSRIWLGTYETPEDAALAYDAAFNMGAKARLNPPLIGSNISG 166  
DB 124 PMGKFAAEIRDPKNGARWLGTFETAEADALAYDAAFRMGRSRLNPLRVNSGEPD 183  
QY 167 PVRVNPKRFPAPFPSTSSSSSSSSSENGGRRKR 202  
DB 184 PVRITSKR---SSSSSSSSSSSTSSSEN--GKLKRR 214

RESULT 8  
US-10-374-780A-2074  
;; Sequence 2074, Application US/10374780A  
;; Publication No. US20040019927A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sherman, Bradley K  
;; APPLICANT: Riechmann, Jose Luis  
;; APPLICANT: Jiang, Cai-Zhong  
;; APPLICANT: Heard, Jacqueline E  
;; APPLICANT: Haake, Volker  
;; APPLICANT: Creelman, Robert A  
;; APPLICANT: Ratcliffe, Oliver  
;; APPLICANT: Adam, Luc J  
;; APPLICANT: Reuber, T. Lynne  
;; APPLICANT: Keddie, James  
;; APPLICANT: Brown, Pierre E  
;; APPLICANT: Pilgrim, Marsha L  
;; APPLICANT: Dubell III, Arnold T  
;; APPLICANT: Pineda, Omaira  
;; APPLICANT: Yu, Guo-Liang  
;; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
;; FILE REFERENCE: MBI-0047 CIP  
;; CURRENT APPLICATION NUMBER: US/10/374,780A  
;; CURRENT FILING DATE: 2003-02-25  
;; PRIOR APPLICATION NUMBER: 09/837,944  
;; PRIOR FILING DATE: 2001-04-18  
;; PRIOR APPLICATION NUMBER: 60/310,847  
;; PRIOR FILING DATE: 2001-08-09  
;; PRIOR APPLICATION NUMBER: 09/934,455  
;; PRIOR FILING DATE: 2001-08-22  
;; PRIOR APPLICATION NUMBER: 60/336,049  
;; PRIOR FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/338,692  
;; PRIOR FILING DATE: 2001-12-11  
;; PRIOR APPLICATION NUMBER: 10/171,468  
;; PRIOR FILING DATE: 2002-06-14  
;; PRIOR APPLICATION NUMBER: 10/225,066  
;; PRIOR FILING DATE: 2002-08-09  
;; PRIOR APPLICATION NUMBER: 10/225,067  
;; PRIOR FILING DATE: 2002-08-09  
;; PRIOR APPLICATION NUMBER: 10/225,068  
;; PRIOR FILING DATE: 2002-08-09  
;; NUMBER OF SEQ ID NOS: 2906  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 2074  
;; LENGTH: 243  
;; TYPE: PRT  
;; ORGANISM: Arabidopsis thaliana  
;; FEATURE:  
;; OTHER INFORMATION: G1006 Paralogous to G28  
US-10-374-780A-2074

Query Match 31.9%; Score 338; DB 15; Length 243;  
Best Local Similarity 39.4%; Pred. No. 5.7e-25;  
Matches 85; Conservative 30; Mismatches 69; Indels 32; Gaps 6;

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Oy      9  SDRFLILIEHLLSDSDSSSELTSTEENMEIIPADFLNMSGSEIQKRG----- 60
Db      9  SDVALLSISTRHLLGGGG-----NELKLNSTBSCTE--SWGGLPLKENSEDMULVYGL 63
Oy      61  -PSSESCQSNMASECOED-----SVGTPEEAAAGGCGSKDMRYKYVRR 106
Db      64  LKDAFHFDPTSSDLSCIFDEPAVKVEPTENFTAMEEKPCKALPVETAVKAGHYGVQR 122
Oy      107  PMGFAEITDPKKKSGRITLGYTEPEDAALAYDAAANMGAGARLNFPILISNLSG 166
Db      124  PMGFAAEIIDPPKNGARVWLGFTEAEDAAALAYDIAARMRGSRALLNFPILVNSGPD 183
Oy      167  PVRVNPKRFPAPETSTSSSSSSSSSSSSSGRKRK 202
Db      184  PVRITSR---SSSSSSSSSSSTSSSEN--GKLKRR 214

RESULT 9
US-10-412-699B-670
/ Sequence 670, Application US/10412699B
/ Publication No. US20040045049A1
/ GENERAL INFORMATION:
/ APPLICANT: Mendel Biotechnology, Inc.
/ APPLICANT: Zhang, James
/ APPLICANT: Fromm, Michael E.
/ APPLICANT: Heard, Jacqueline B.
/ APPLICANT: Riechmann, Jose Luis
/ APPLICANT: Adam, Luc J.
/ APPLICANT: Broun, Pierre E.
/ APPLICANT: Pineda, Omaisra
/ APPLICANT: Reuber, T. Lynne
/ APPLICANT: Keddie, James S.
/ APPLICANT: Yu, Guo-liang
/ APPLICANT: Ujang, Cai-Zhong
/ APPLICANT: Samaha, Raymond R.
/ APPLICANT: Pilgrim, Marsha L.
/ APPLICANT: Creelman, Robert A.
/ APPLICANT: Dubell, Arnold N.
/ APPLICANT: Ratcliffe, Oliver
/ APPLICANT: Kumimoto, Rodetrick
/ APPLICANT: Sherman, Bradley K.
/ TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
/ FILE REFERENCE: MBI-0048CIP
/ CURRENT APPLICATION NUMBER: US/10/412,699B
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: 09/394,519
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: 09/489,376
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: 09/506,720
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 09/533,030
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,392
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,029
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/532,591
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,648
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/713,994
/ PRIOR FILING DATE: 2000-11-16
/ PRIOR APPLICATION NUMBER: 09/819,142
/ PRIOR FILING DATE: 2001-03-27
/ Remaining SEQ ID Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2011
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 670
/ LENGTH: 243
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana

```

```
; FEATURE INFORMATION: GJ006
; OTHER INFORMATION: US-10-412-699B-670

Query Match      31.9%; Score 338; DB 15; Length 243;
Best Local Similarity    39.4%; Pred. No. 5,7e-25;
Matches   85; Conservative     30; Mismatches    69; Indels     32; Gaps       6;

QY          SDRFLSLIEHLLSDNSDDSSSELTSTEENWEELPADFLNWSGSELQRGS-----        60
           ||||| | |||| : ||| | | | | | | | | | | | | | | | | | | | | | |
DB          SDVALLEISITHLGGGE---NEILRNESTPSCFTE--SWGGLPLENDSEDMLVYLX    63

OY         61 -PSESQSNSMASSCOED-----SVGTPEPAAGGCCKDMRKYGVARR    106
           ::::: ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB         64 LKDAHFHEPTSSDISCLDFEPFAVKVEPTENTAMEEKKKALPTETRVAKAHIGVROR    123
           ||||||| ||||| | | | | | | | | | | | | | | | | | | | | | | |

OY         107 PWGFPAEIRPPKKGRIMWTGETEPEDAALAAYDAAAFNNRGAKARLPFHLSGNISG    166
            ||||||| ||||| | | | | | | | | | | | | | | | | | | | | | | |
DB         124 PWCFFAEEIRPDANGARVMWLGTFETMEDALADIAAFRRRGSRALLNPPLRVNVSGSPD    183
            ||||||| ||||| | | | | | | | | | | | | | | | | | | | | | | |

OY         167 PVRVNPRKRFPAPSTTTSRSSSSSENSGGRKKXR    202
           ||| : : : | : | : | | | | | | | | | | | | | | | |
DB         184 PVRTSKR----SSSSSSSSSSTSSEER-GKLXRR    214
           ||| : : : | : | : | | | | | | | | | | | | | | | |

RESULT 10
US-10-412-699B-183Z
; Sequence 183Z, Application US/10412699B
; Publication No., USP0040045049A1
GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline B.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Brown, Pierre E.
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond K.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: Dubell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kumamoto, Rogerick
; APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MB1-0048CIP
CURRENT APPLICATION NUMBER: US/10/412,699B
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,591
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,648
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/713,994
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/819,142
PRIOR FILING DATE: 2001-03-27
```

```

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1832
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-412-699B-1832

Query Match
  31.9%; Score 338; DB 15; Length 243;
Best Local Similarity 39.4%; Pred. No. 5.7e-25;
Matches 85; Conservative 30; Mismatches 69; Indels 32; Gaps 6;

QY 9 SDRFLSLIEHLSDNSDSSSELTSTEENWEIIPADFLWVSGSEIQKGS-----60
DB 9 SDYALLESTRHLGGGGE---NEURLNTESTPSSCFTE--SWGGLPLKENSSEDMLVYGL 63
QY 61 -SSSECCQSNMAESQED-----SVVGTPEAAAGGCGCKDMRRYGVRR 106
DB 64 LKDAFHFDTSDDLCLFDPFAVKVEPTENFTAMEEKPKKALPVETAVKAKHYGVRR 123
QY 107 PMGKFAAEIRDPKKGSRIMLGTYETPEDALAYDAAAFNNRGAKARLNFPHLIGSNISG 166
DB 124 PMGKFAAEIRDPKKGARVWLGTFTAEEDALAYDIAAFNRGSRALLNPLRVNSGEPD 183
QY 167 PVRVNRKRFPAEPSTTSSSSSSSSSSSGGRRKR 202
DB 184 PVRITSKR---SSSSSSSSSSSTSSSEN--GTLKR 214

RESULT 11
US-10-425-114-41687
; Sequence 41687, Application US/10425114
; Publication No. US20040034888A1
GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41687
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB25-108-B7_FLI.pep
US-10-425-114-41687

Query Match
  31.9%; Score 338; DB 15; Length 248;
Best Local Similarity 39.4%; Pred. No. 5.8e-25;
Matches 85; Conservative 30; Mismatches 69; Indels 32; Gaps 6;

QY 9 SDRFLSLIEHLSDNSDSSSELTSTEENWEIIPADFLWVSGSEIQKGS-----60
DB 14 SDYALLESTRHLGGGGE---NEURLNTESTPSSCFTE--SWGGLPLKENSSEDMLVYGL 68
QY 61 -SSSECCQSNMAESQED-----SVVGTPEAAAGGCGCKDMRRYGVRR 106
DB 69 LKDAFHFDTSDDLCLFDPFAVKVEPTENFTAMEEKPKKALPVETAVKAKHYGVRR 128
QY 107 PMGKFAAEIRDPKKGSRIMLGTYETPEDALAYDAAAFNNRGAKARLNFPHLIGSNISG 166
DB 129 PMGKFAAEIRDPKKGARVWLGTFTAEEDALAYDIAAFNRGSRALLNPLRVNSGEPD 188
QY 167 PVRVNRKRFPAEPSTTSSSSSSSSSGGRRKR 202
DB 184 PVRITSKR---SSSSSSSSSSSTSSSEN--GTLKR 214
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DB 189 PVRITSKR---SSSSSSSSSSSTSSSEN--GTLKR 219

RESULT 12
US-10-424-599-208822
; Sequence 208822, Application US/10424599
; Publication No. US20040031072A1
GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 208822
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_30595C.1.pep
US-10-424-599-208822

Query Match
  31.3%; Score 331.5; DB 15; Length 156;
Best Local Similarity 52.1%; Pred. No. 1.4e-24;
Matches 73; Conservative 14; Mismatches 38; Indels 15; Gaps 3;

QY 30 SSELSTENWEIIPADFLWVSGSEI---QKRGSSSSSCQSNK-ASCCQEDSVYGV 84
DB 2 SSTTSDSCYCLEQIOQYVLLHNDSTILTPQAPSPSSSHSSDASVHPHPEADHVNAP 61
QY 85 PEAAAGCGCKDMRRYGVRRPMGKFAAEIRDPKKGSRIMLGTYETPEDALAYDAA 144
DB 62 PK-----RRRYGVRRPMGKFAAEIRDPKKGSRVWLGTVNEEADALAYDKA 111
QY 145 FNNRGAKARLNFPHLIGSN 164
DB 112 FNNRGQKAKLNFPHLIGSCV 131

RESULT 13
US-10-425-114-43402
; Sequence 43402, Application US/10425114
; Publication No. US20040034888A1
GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43402
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700237304_FLI.pep
US-10-425-114-43402

Query Match
  31.2%; Score 330.5; DB 15; Length 311;
Best Local Similarity 36.9%; Pred. No. 4.4e-24;
Matches 90; Conservative 29; Mismatches 54; Indels 71; Gaps 11;

QY 9 SDRFLSLIEHLSDNSDSSSELTSTEENWEIIPADFLWVSGS-----53
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Db 42 SETSVLDTIRQHLL---EEPAABAPADESPGSLVAD---QWSSSLFRTDDADDMWVFG 96
QY 54 EIQKR-----GS-----PSSSCOSNMAESCOEDSVVGT-----84
Db 97 VLQDAFAYGWLPGSFPVHVXPEPVRSPPSSSYHPCSYD---GSPCFGLDPEPLTPGTT 153
QY 85 -----PEAAGGCGSKDMRYKGVRRPMPGKFAAEIRDPKKGSRIWLTGYETPEPAAL 138
Db 154 TPGGGEAAAMARGL---HYRGVRRPMPGKFAAEIRDPKNGARVWLGTDTAEPAAL 210
QY 139 AYDAAFNMKGAKARLNFPHLIGSNISGPVVRPKRFPAPESPSTSSSSSSSSSSSGR 198
Db 211 AYRAAAYRMKGRSLALNPLRIG---SGDKRPSRA---PEPATSSDSSSSA---SGSH 260
QY 199 KKR 202
Db 261 KRRK 264

RESULT 14
US-09-533-029-18
; Sequence 18, Application US/09533029
; Publication No. US20030046723A1
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddle, James
; APPLICANT: Pineda, Omaisra
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G28
US-09-533-029-18

Query Match 30.6%; Score 324; DB 10; Length 268;
Best Local Similarity 36.0%; Pred. No. 1.6e-23;
Matches 91; Conservative 27; Mismatches 69; Indels 66; Gaps 9;

QY 1 MSEIISVSDRFLSLIEHLSDN-----SDSSSELST-----36
Db 1 MSMTADSQDYAFLESIRRLHGESEPILESTASSVTGSCVYGQSIKPYGRRNPFSKL 60
QY 37 -----EENW-----EBIFADFL-----NW-----SGSEIQKRGSPS--SESCQSN 69
Db 61 YPCFTESWGLPLKENDSEBMLVYGILNDAFHGGEWEPSSSSSDDEDRSPSVKLETPESEF 120
QY 70 SMAESCOEDSVGTPEPAAAGCGSKDMRYKGVRRPMPGKFAAEIRDPKKGSRIWLT 129
Db 121 AAVDSVPVKKKTSPPVSAATAAGK---HYRGVRRPMPGKFAAEIRDPKNGARVWLGT 177
QY 130 YETPEDAALAYDAAFNMKGAKARLNFPHLIGSNISGPVVRPKRFPAPESPSTSSSSSS 189
Db 178 FETAEADAALAYDAAFNMKGRSLALNPLRIGSNISGPVVRPKRFPAPESPSTSSSSSS 226
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QY 190 SSENSEGGRRKR 202
Db 227 SSNEN-GAPKKR 238

RESULT 15
US-09-934-455-2
; Sequence 2, Application US/09934455
; Publication No. US20030121070A1
; GENERAL INFORMATION:
; APPLICANT: Adam, Luc
; APPLICANT: Creelman, Robert
; APPLICANT: Dubell, Arnold
; APPLICANT: Heard, Jacqueline
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Keddle, James
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Reuber, Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Pineda, Omaisra
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV
; FILE REFERENCE: MBI-0025
; CURRENT APPLICATION NUMBER: US/09/934,455
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: MBI-0022
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: MBI-0023
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-934-455-2

Query Match 30.6%; Score 324; DB 10; Length 268;
Best Local Similarity 36.0%; Pred. No. 1.6e-23;
Matches 91; Conservative 27; Mismatches 69; Indels 66; Gaps 9;

QY 1 MSEIISVSDRFLSLIEHLSDN-----SDSSSELST-----36
Db 1 MSMTADSQDYAFLESIRRLHGESEPILESTASSVTGSCVYGQSIKPYGRRNPFSKL 60
QY 37 -----EENW-----EBIFADFL-----NW-----SGSEIQKRGSPS--SESCQSN 69
Db 61 YPCFTESWGLPLKENDSEBMLVYGILNDAFHGGEWEPSSSSSDDEDRSPSVKLETPESEF 120
QY 70 SMAESCOEDSVGTPEPAAAGCGSKDMRYKGVRRPMPGKFAAEIRDPKKGSRIWLT 129
Db 121 AAVDSVPVKKKTSPPVSAATAAGK---HYRGVRRPMPGKFAAEIRDPKNGARVWLGT 177
QY 130 YETPEDAALAYDAAFNMKGAKARLNFPHLIGSNISGPVVRPKRFPAPESPSTSSSSSS 189
Db 178 FETAEADAALAYDAAFNMKGRSLALNPLRIGSNISGPVVRPKRFPAPESPSTSSSSSS 226
QY 190 SSENSEGGRRKR 202
Db 227 SSNEN-GAPKKR 238
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Search completed: February 27, 2005, 22:20:33  
Job time : 131 secs

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QY 167 PVAVNPKRPPAEPSTSSSSSSSSSSSGGKRR 202  
DB 184 PVRTSKR---SSSSSSSSSSSSSTSSSEN--GKLKRR 214

## RESULT 2

US-09-533-029-18  
; Sequence 18, Application US/09533029  
; Patent No. 6664446  
; GENERAL INFORMATION:  
; APPLICANT: Heard, Jacqueline  
; APPLICANT: Brown, Pierre  
; APPLICANT: Kiechmann, Jose-Luis  
; APPLICANT: Keddle, James  
; APPLICANT: Pineda, Omatra  
; APPLICANT: Adam, Luc  
; APPLICANT: Samaha, Raymond  
; APPLICANT: Zhang, James  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ralccliffe, Oliver  
; APPLICANT: Pilgrim, Marsha  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Reuber, Lynne  
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES  
; FILE REFERENCE: MB1-010  
; CURRENT APPLICATION NUMBER: US/09/533,029  
; CURRENT FILING DATE: 2000-03-22  
; EARLIER APPLICATION NUMBER: 60/125,814  
; EARLIER FILING DATE: 1999-03-23  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; OTHER INFORMATION: G28  
US-09-533-029-18

## Query Match

Best Local Similarity 30.6%; Score 324; DB 4; Length 268;  
Best Local Similarity 36.0%; Pred. No. 1.5e-28;  
Matches 91; Conservative 27; Mismatches 69; Indels 66; Gaps 9;

QY 1 MSEIISVSDRPLSLIBHLSDN---SDSSSELSTST----- 36  
DB 1 MSMTADSQSDYALFLESIRHLGSESEPISESTASVTOSCTYGOSIKRYGARNPSFKL 60  
QY 37 -----BNW-----EIPADFL-----NW-----SGSEIQKRGSPS--SSCOSN 69  
DB 61 YPCFTSWCDLPLKENDSEMDLVYGILNDAFHGWPSSSSSDSDERSSPSVKIEPESF 120  
QY 70 SMAESQOEDSVGTPPEAAAGCGCKDMNRKYGVRPRPKFAAEIRDKKKSGRIWGT 129  
DB 121 AAVDSVPVKKKETSVPVSAATTAAGK--HYRGVRPRPKFAAEIRDKKGAARWLG 177  
QY 130 YETPEDAALAYDAAAFNRGAKARLNFPHLIGSNTSGPVRVPRKRPAPETSSSSSS 189  
DB 178 FETAEADALAYDAAAFNRGSRALLNPLRVNSGEPDPVRIKSR-----SSFS 226  
QY 190 SSENSEGGKRR 202  
DB 227 SSNN--GAPKRR 238

## RESULT 3

US-09-202-161B-1  
; Sequence 1, Application US/09202161B  
; Patent No. 6653533  
; GENERAL INFORMATION:  
; APPLICANT: Purdue Research Foundation  
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS  
; FILE REFERENCE: 7024-371  
; CURRENT APPLICATION NUMBER: US/09/202,161B

; CURRENT FILING DATE: 1999-06-14  
; PRIOR APPLICATION NUMBER: PCT/US97/10382  
; PRIOR FILING DATE: 1997-06-12  
; PRIOR APPLICATION NUMBER: 60/046,494  
; PRIOR FILING DATE: 1997-05-14  
; PRIOR APPLICATION NUMBER: 60/019,633  
; PRIOR FILING DATE: 1996-06-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: ASCII  
; SEQ ID NO 1  
; LENGTH: 231  
; TYPE: PRT  
; ORGANISM: Lycopersicon esculentum  
US-09-202-161B-1

## Query Match

Best Local Similarity 28.2%; Score 298.5; DB 4; Length 231;  
Best Local Similarity 43.5%; Pred. No. 1e-25;  
Matches 67; Conservative 18; Mismatches 50; Indels 19; Gaps 3;

QY 49 NMSGSEIQKRGSPSSSCSNMAESQOEDSVGTPPEAAAGCGCKDMNRKYGVRPRP 108  
DB 65 NFTAQGVKSEPRREIESSEPSF-----PSPAGT---TAAPAEIRPKGRHRYGVQRW 114  
QY 109 GKFAAEIRDPKKGSRWLTGTETPEDAALAYDAAAFNRGAKARLNFPHLIGSNTSGV 168  
DB 115 GKFAAEIRDPKAGARWLTGTETAEBAALAYDKAAYRRGSKXHLNFPHRIGLNEPDP 174  
QY 169 RVNPKRPPAEPSTSSSSSSSSSSSGGKRR 202  
DB 175 ELRRKRAIOGP-----ASSSGNSKRR 199

## RESULT 4

US-08-912-272-18  
; Sequence 18, Application US/08912272  
; Patent No. 6093874  
; GENERAL INFORMATION:  
; APPLICANT: Jofuku, K. Diane  
; APPLICANT: Okamoto, Jack K.  
; TITLE OF INVENTION: Methods for Improving Seeds  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,272  
; FILING DATE: 15-AUG-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/879,827  
; FILING DATE: 20-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/700,152  
; FILING DATE: 20-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baebian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-067220US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 amino acids



```

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..69
; OTHER INFORMATION: /note="AP2 domain within tobacco
; OTHER INFORMATION: ERBP-2"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 35..51
; OTHER INFORMATION: /note="putative ERBP-2 amphipathic
; OTHER INFORMATION: alpha-helix"
; US-08-912-272-18

Query Match 25.9%; Score 274; DB 3; Length 69;
Best Local Similarity 76.6%; Pred. No. 1e-23;
Matches 49; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 100 YKGVRRPVGKFAEIRDPKKGSRVWLGTYETPEDAALAYDAAFNMGAKARLNFPH 159
DB 4 YRGVRRPVGKFAEIRDPKKGSRVWLGTYETPEDAALAYDAAFNMGAKARLNFPHR 63
QY 160 IGSN 163
DB 64 IGLN 67

RESULT 5
US-09-026-039-18
; Sequence 18, Application US/09026039
; Patent No. 6329567
; GENERAL INFORMATION:
; APPLICANT: Jofuku, K. Diane
; APPLICANT: Okamura, Jack K.
; TITLE OF INVENTION: Methods for Improving Seeds
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,039
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,272
; FILING DATE: 15-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/879,827
; FILING DATE: 20-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/700,152
; FILING DATE: 20-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-067230US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 amino acids
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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..69
; OTHER INFORMATION: /note="AP2 domain within tobacco
; OTHER INFORMATION: ERBP-2"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 35..51
; OTHER INFORMATION: /note="putative ERBP-2 amphipathic
; OTHER INFORMATION: alpha-helix"
; US-09-026-039-18

Query Match 25.9%; Score 274; DB 3; Length 69;
Best Local Similarity 76.6%; Pred. No. 1e-23;
Matches 49; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 100 YKGVRRPVGKFAEIRDPKKGSRVWLGTYETPEDAALAYDAAFNMGAKARLNFPH 159
DB 4 YRGVRRPVGKFAEIRDPKKGSRVWLGTYETPEDAALAYDAAFNMGAKARLNFPHR 63
QY 160 IGSN 163
DB 64 IGLN 67

RESULT 6
US-09-300-672-9
; Sequence 9, Application US/09300672
; Patent No. 6248937
; GENERAL INFORMATION:
; APPLICANT: Finkelstein, Ruth R.
; APPLICANT: Lynch, Tim
; APPLICANT: Goodman, Howard M.
; APPLICANT: Wang, Ming-Li
; TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,
; FILE REFERENCE: 480.89 (HV)
; CURRENT APPLICATION NUMBER: US/09/300,672
; CURRENT FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 60
; TYPE: PRT
; ORGANISM: AP2 domain protein
; US-09-300-672-9

Query Match 25.1%; Score 266; DB 3; Length 60;
Best Local Similarity 78.0%; Pred. No. 6.7e-23;
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRPVGKFAEIRDPKKGSRVWLGTYETPEDAALAYDAAFNMGAKARLNFPH 158
DB 1 YRGVRRPVGKFAEIRDPKKGSRVWLGTYETPEDAALAYDAAFNMGAKARLNFPHR 59

RESULT 7
US-09-202-161B-2
; Sequence 2, Application US/09202161B
; Patent No. 6653533
; GENERAL INFORMATION:
; APPLICANT: Purdue Research Foundation
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: 7024-371
; CURRENT APPLICATION NUMBER: US/09/202,161B
; CURRENT FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: PCT/US97/10382
; PRIOR FILING DATE: 1997-06-12
; PRIOR APPLICATION NUMBER: 60/046,494
```

PRIOR FILING DATE: 1997-05-14  
PRIOR APPLICATION NUMBER: 60/019, 633  
PRIOR FILING DATE: 1996-06-12  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: ASCII  
SEQ ID NO 2  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Lycopersicon esculentum  
US-09-202-161B-2

Query Match 25.1%; Score 266; DB 4; Length 161;  
Best Local Similarity 55.6%; Pred. No. 3e-22;  
Matches 55; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

QY 99 RYGVRRRPMGKFAAIRDPPKKGSRIWLTETPEDALAYDAAPFNRGAKALNFP 158  
DB 58 KYGVRRRPMGKFAAIRDPAKNGARVWLTETPEAEALAYDAAPFNRGAKALNFP 117

QY 159 LIGSNISGPRVNPFRKFPAPSPPTSSSSSSSSSSSSG 197  
DB 118 EI---VNASVSD-KSLCSNSYTTNNSSSLNEVSSG 152

RESULT 8  
US-08-949-603-11  
Sequence 11, Application US/08949603  
Patent No. 5891859

GENERAL INFORMATION:  
APPLICANT: Michael F. Thomashow and

TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
TITLE OF INVENTION: WHICH REGULATES COLD AND  
TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS 5.00  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/949,603  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/706,270  
FILING DATE: September 4, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod

REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-384  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5891859e  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61  
TYPE: Amino Acid  
STRANDEDNESS: Single

TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: Tobacco  
STRAIN:  
INDIVIDUAL ISOLATE: N/A  
DEVELOPMENTAL STAGE: N/A  
HAPLOTYPE: N/A  
TISSUE TYPE: N/A  
CELL TYPE: N/A  
CELL LINE: N/A  
ORGANELLE: N/A

IMMEDIATE SOURCE: N/A  
POSITION IN GENOME: N/A  
FEATURE:

NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD: sequencing  
OTHER INFORMATION: Figure 2D  
PUBLICATION INFORMATION:  
US-08-949-603-11

Query Match 24.8%; Score 262; DB 2; Length 61;  
Best Local Similarity 78.0%; Pred. No. 2e-22;  
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRRPMGKFAAIRDPPKKGSRIWLTETPEDALAYDAAPFNRGAKALNFP 158  
DB 2 YRGVRRRPMGKFAAIRDPAKNGARVWLTETPEAEALAYDAAPFNRGAKALNFP 60

RESULT 9  
US-08-706-270A-11  
Sequence 11, Application US/08706270A  
Patent No. 5892009

GENERAL INFORMATION:  
APPLICANT: Michael F. Thomashow and  
APPLICANT: Eric J. Stockinger  
TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
TITLE OF INVENTION: WHICH REGULATES COLD AND  
TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS 5.00  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/706,270A  
FILING DATE: September 4, 1996  
CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod

REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-310  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5892009e  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61  
TYPE: Amino Acid  
STRANDEDNESS: Single

TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHEICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: Tobacco  
STRAIN:  
INDIVIDUAL ISOLATE: N/A  
DEVELOPMENTAL STAGE: N/A  
HAPLOTYPE: N/A  
TISSUE TYPE: N/A  
CELL TYPE: N/A  
CELL LINE: N/A  
ORGANELLE: N/A  
IMMEDIATE SOURCE: N/A  
POSITION IN GENOME: N/A  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD: sequencing  
OTHER INFORMATION: Figure 2D  
PUBLICATION INFORMATION:  
US-08-706-270A-11

Query Match 24.8%; Score 262; DB 2; Length 61;  
Best Local Similarity 78.0%; Pred. No. 2e-22;  
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRPMPGKFAEIRDPKKGSRIMLTGTEPDPALAYDAAFNMGAKARLNPPH 158  
DB 2 YKGVRRPMPGKFAEIRDPKKGSRIMLTGTEPDPALAYDAAFNMGAKARLNPPH 60

RESULT 10  
US-08-949-580-11  
Sequence 11, Application US/08949580  
Patent No. 5929305

GENERAL INFORMATION:  
APPLICANT: Michael F. Thomashow and  
APPLICANT: Eric J. Stockinger  
TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
TITLE OF INVENTION: WHICH REGULATES COLD AND  
TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS 5.00  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/949,580  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/706,270  
FILING DATE: September 4, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5929305e

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:

LENGTH: 61  
TYPE: Amino Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHEICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: Tobacco  
STRAIN:

INDIVIDUAL ISOLATE: N/A  
DEVELOPMENTAL STAGE: N/A  
HAPLOTYPE: N/A  
TISSUE TYPE: N/A  
CELL TYPE: N/A  
CELL LINE: N/A  
ORGANELLE: N/A  
IMMEDIATE SOURCE: N/A  
POSITION IN GENOME: N/A  
FEATURE:

NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD: sequencing  
OTHER INFORMATION: Figure 2D  
PUBLICATION INFORMATION:  
US-08-949-580-11

Query Match 24.8%; Score 262; DB 2; Length 61;  
Best Local Similarity 78.0%; Pred. No. 2e-22;  
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRPMPGKFAEIRDPKKGSRIMLTGTEPDPALAYDAAFNMGAKARLNPPH 158  
DB 2 YKGVRRPMPGKFAEIRDPKKGSRIMLTGTEPDPALAYDAAFNMGAKARLNPPH 60

RESULT 11  
US-08-950-172A-11  
Sequence 11, Application US/08950172A  
Patent No. 5965705

GENERAL INFORMATION:  
APPLICANT: Michael F. Thomashow and  
APPLICANT: Eric J. Stockinger  
TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
TITLE OF INVENTION: WHICH REGULATES COLD AND  
TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS 5.00  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/950,172A  
FILING DATE: 10/14/1997

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/949,580  
FILING DATE: October 14, 1997  
APPLICATION NUMBER: 08/706,270  
FILING DATE: September 4, 1996  
ATTORNEY/AGENT INFORMATION:

NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 59657056  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61  
TYPE: Amino Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: Tobacco  
STRAIN:  
INDIVIDUAL ISOLATE: N/A  
DEVELOPMENTAL STAGE: N/A  
HAPLOTYPE: N/A  
TISSUE TYPE: N/A  
CELL TYPE: N/A  
CELL LINE: N/A  
ORGANELLE: N/A  
IMMEDIATE SOURCE: N/A  
POSITION IN GENOME: N/A  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD: sequencing  
OTHER INFORMATION: Figure 2D  
PUBLICATION INFORMATION:  
US-08-950-172A-11

Query Match 24.8%; Score 262; DB 2; Length 61;  
Best Local Similarity 78.0%; Pred. No. 2e-22;  
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRPVGKFAAEIRDPKKGSRIMLTGTYETPEDALAYDAAFNMGAKARLNFPH 158  
DB 2 YRGVRRPVGKFAAEIRDPKKGSRIMLTGTYETPEDALAYDAAFNMGAKARLNFPH 60

RESULT 12  
US-09-198-119C-11  
Sequence 11, Application US/09198119C  
Patent No. 6417428  
GENERAL INFORMATION:  
APPLICANT: Thomashow, Michael  
APPLICANT: Stockinger, Eric  
APPLICANT: Jaglo-Octosen, Kirsten  
APPLICANT: Gilmour, Sarah  
APPLICANT: Zarka, Daniel  
APPLICANT: Jiang, Cai-Zhong  
TITLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance  
FILE REFERENCE: 19117,713 Seq List  
CURRENT APPLICATION NUMBER: US/09198,119C  
PRIOR FILING DATE: 1998-11-23  
PRIOR APPLICATION NUMBER: US 08/706,270  
PRIOR FILING DATE: 1998-09-04  
PRIOR APPLICATION NUMBER: US 09/018,233  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: US 09/017,816  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: US 09/018,235  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: US 09/017,575  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: US 09/018,227  
PRIOR FILING DATE: 1998-02-03

PRIOR APPLICATION NUMBER: US 09/018,234  
PRIOR FILING DATE: 1998-02-03  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: Patencin Ver. 2.0  
SEQ ID NO 11  
LENGTH: 61  
TYPE: PRT  
ORGANISM: Nicotiana tabacum  
US-09-198-119C-11

Query Match 24.8%; Score 262; DB 4; Length 61;  
Best Local Similarity 78.0%; Pred. No. 2e-22;  
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRPVGKFAAEIRDPKKGSRIMLTGTYETPEDALAYDAAFNMGAKARLNFPH 158  
DB 2 YRGVRRPVGKFAAEIRDPKKGSRIMLTGTYETPEDALAYDAAFNMGAKARLNFPH 60

RESULT 13  
US-09-601-802D-11  
Sequence 11, Application US/09601802D  
Patent No. 6706866  
GENERAL INFORMATION:  
APPLICANT: Thomashow, Michael  
APPLICANT: Stockinger, Eric  
APPLICANT: Jaglo-Octosen, Kirsten  
APPLICANT: Gilmour, Sarah  
APPLICANT: Zarka, Daniel  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Zhang, James  
APPLICANT: Haake, Volker  
TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL  
TITLE OF INVENTION: STRESS TOLERANCE  
FILE REFERENCE: 514442000201/MB10029  
CURRENT APPLICATION NUMBER: US/09/601,802D  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/018,233  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/017,816  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/018,235  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/017,575  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/018,227  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/018,234  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/198,119  
PRIOR FILING DATE: 1998-11-23  
NUMBER OF SEQ ID NOS: 259  
SOFTWARE: PatsSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 61  
TYPE: PRT  
ORGANISM: Nicotiana tabacum  
US-09-601-802D-11

Query Match 24.8%; Score 262; DB 4; Length 61;  
Best Local Similarity 78.0%; Pred. No. 2e-22;  
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRPVGKFAAEIRDPKKGSRIMLTGTYETPEDALAYDAAFNMGAKARLNFPH 158  
DB 2 YRGVRRPVGKFAAEIRDPKKGSRIMLTGTYETPEDALAYDAAFNMGAKARLNFPH 60

RESULT 14  
US-09-601-802D-134  
Sequence 134, Application US/09601802D  
Patent No. 6706866  
GENERAL INFORMATION:

APPLICANT: Thomashow, Michael  
APPLICANT: Stockinger, Eric  
APPLICANT: Jaglo-Ottosen, Kirsten  
APPLICANT: Gilmour, Sarah  
APPLICANT: Zarika, Daniel  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Zhang, James  
APPLICANT: Haake, Volker  
TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL  
STRESS TOLERANCE  
FILE REFERENCE: 51442000201/MB10029  
CURRENT APPLICATION NUMBER: US/09/601,802D  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/018,233  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/017,816  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/018,235  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/017,575  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/018,227  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/018,234  
PRIOR FILING DATE: 1998-02-03  
PRIOR APPLICATION NUMBER: 09/198,119  
PRIOR FILING DATE: 1998-11-23  
NUMBER OF SEQ ID NOS: 259  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 134  
LENGTH: 63  
TYPE: PRT  
ORGANISM: Nicotiana tabacum  
US-09-601-802D-134

Query Match 24.8%; Score 262; DB 4; Length 63;  
Best Local Similarity 78.0%; Pred. No. 2,1e-22;  
Matches 46; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRPMPGKFAEIRDPKKGSRWLGYETPEDAALAYDAAFMNGAKARLNPF 158  
DB 4 YRGVRRPMPGKFAEIRDPKKGSRWLGYETPEDAALAYDAAFMNGAKARLNPF 62

US-08-912-272-17  
Sequence 17, Application US/08912272  
Patent No. 6093874  
GENERAL INFORMATION:  
APPLICANT: Jofuku, K. Diane  
APPLICANT: Okamoto, Jack K.  
TITLE OF INVENTION: Methods for Improving Seeds  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,272  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/879,827  
FILING DATE: 20-JUN-1997  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/700,152  
FILING DATE: 20-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Baselian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-067220US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..69  
OTHER INFORMATION: /note="AP2 domain within tobacco  
ERBP-1"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 36..51  
OTHER INFORMATION: /note="putative ERBP-1 amphipathic  
alpha-helix"  
US-08-912-272-17

Query Match 24.4%; Score 258; DB 3; Length 69;  
Best Local Similarity 77.6%; Pred. No. 6,9e-22;  
Matches 45; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 100 YKGVRRPMPGKFAEIRDPKKGSRWLGYETPEDAALAYDAAFMNGAKARLNPF 157  
DB 4 YRGVRRPMPGKFAEIRDPKKGSRWLGYETPEDAALAYDAAFMNGAKARLNPF 61

Search completed: February 27, 2005, 22:07:39  
Job time: 44 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 27, 2005, 22:07:45 ; Search time 174 seconds

(without alignments)  
597,426 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 203

Sequence: 1 MSEERISVSDRFLSLIEHL.....SSSSSSSSSENSGGRKKRY 203

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	203	100.0	203	2	Q9LDB6	Q9LDB6 catharanthu
2	19	9.4	202	2	Q8LIR3	Q8LIR3 glycine max
3	19	9.4	226	2	O22167	O22167 arabidopsis
4	19	9.4	226	2	Q8L9K1	Q8L9K1 arabidopsis
5	18	8.9	210	2	Q9LEH6	Q9LEH6 catharanthu
6	17	8.4	124	2	Q7XDZ2	Q7XDZ2 oryza sativ
7	17	8.4	128	2	Q6WVK9	Q6WVK9 oryza sativ
8	17	8.4	139	2	Q9LTC5	Q9LTC5 arabidopsis
9	17	8.4	165	2	Q75UJ5	Q75UJ5 cucumis mel
10	17	8.4	201	2	Q8LDL4	Q8LDL4 arabidopsis
11	17	8.4	201	2	Q84XB0	Q84XB0 lycopersico
12	17	8.4	201	2	Q9FKG2	Q9FKG2 arabidopsis
13	17	8.4	204	2	Q6V5F2	Q6V5F2 capeella ru
14	17	8.4	206	2	Q6V5U8	Q6V5U8 brassica ol
15	17	8.4	207	2	Q6V5B8	Q6V5B8 arabidopsis
16	17	8.4	207	2	Q6V5D3	Q6V5D3 olimmarido
17	17	8.4	207	2	Q6V5G9	Q6V5G9 arabidopsis
18	17	8.4	207	2	Q9LYO5	Q9LYO5 arabidopsis
19	17	8.4	208	2	Q6WEP6	Q6WEP6 boechera dr
20	17	8.4	218	2	Q6V5I2	Q6V5I2 silymbrium
21	17	8.4	236	2	Q40476	Q40476 nicotiana t
22	17	8.4	278	2	Q6RZW8	Q6RZW8 vitis aesci
23	17	8.4	282	2	Q9MAY9	Q9MAY9 mesembryant
24	17	8.4	292	2	Q94DB4	Q94DB4 oryza sativ
25	16	7.9	127	2	Q9AC14	Q9AC14 brassica ol
26	16	7.9	131	2	Q651A5	Q651A5 oryza sativ
27	16	7.9	218	2	Q8LDC8	Q8LDC8 arabidopsis
28	16	7.9	218	2	Q9ZNR2	Q9ZNR2 arabidopsis
29	16	7.9	240	2	Q8H6S9	Q8H6S9 lycopersico
30	16	7.9	245	2	Q8GZE9	Q8GZE9 lycopersico
31	16	7.9	277	2	P93392	P93392 nicotiana t

## ALIGNMENTS

RESULT 1									
ID	Q9LDB6	PRELIMINARY;	PRT;	203 AA.					
AC	Q9LDB6								
DT	01-OCT-2000 (Tremblrel. 15, Created)								
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)								
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)								
DE	AP2-domain DNA-binding protein.								
GN	Name=orca3;								
OS	Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).								
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;								
OC	lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae;								
OC	Catharanthus.								
OX	NCBI_TaxID=4058;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=G-dom; TISSUE=Root;								
RX	MEDLINE=20355201; PubMed=10894776; DOI=10.1126/science.289.5477.295;								
RA	van der Fits L., Memelink D.;								
RT	"ORCA3, a jasmonate-responsive transcriptional regulator of plant								
RT	primary and secondary metabolism."								
RL	Science 289:295-297(2000).								
DR	EMBL; AJ251250; CAB96900.1; -								
DR	EMBL; AJ251249; CAB96899.1; -								
DR	HSSP; O80337; 2GCC.								
DR	TRANSFAC; T04751; -								
DR	GO; GO:0005634; C:nucleus; IEA.								
DR	GO; GO:0003700; F:transcription factor activity; IEA.								
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.								
DR	InterPro; IPR001471; TF_ERF.								
DR	PRINTS; PR00367; ETHRSPLEMT.								
DR	Prodom; PD001423; TF_ERF; 1.								
KW	SMART; SM00380; AP2; 1.								
KW	DNA-binding.								
SO	SEQUENCE	203 AA;	22322 MW;	CEE84C274312A601 CRC64;					
Query Match									
Best Local Similarity 100.0%; Score 203; DB 2; Length 203;									
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	MSEERISVSDRFLSLIEHLISDNDSSSELTSTEENWEIRFADFLNWSGSEIQKGS	60						
QY	61	PSSESQSNMAESCOEDSVGTPPEAAGGCGSKDMNRYKGVRRPWGKFAEIRDPK	120						
DB	61	PSSESQSNMAESCOEDSVGTPPEAAGGCGSKDMNRYKGVRRPWGKFAEIRDPK	120						
QY	121	KGSRIWLTGTEPEDAALAYDAAFNMGAKALNPFHLIGSNISGVPVNPVKRFPAPB	180						
DB	121	KGSRIWLTGTEPEDAALAYDAAFNMGAKALNPFHLIGSNISGVPVNPVKRFPAPB	180						
QY	181	STTSSSSSSSENSGGRKKRY 203							

```

Db      181 STSSSSSSSSSSSSSGRRKRRY 203
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RESULT 2
ID      08L9R3      PRELIMINARY;      PRT;      202 AA.
AC      08L9R3;
DT      01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT      01-OCT-2002 (T-EMBLrel. 26, Last annotation update)
DE      Ethylene-responsive element binding protein 1.
GN      Name=EREBP1.
OS      Glycine max (Soybean).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosid II; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX      NCB1_TaxId=3847;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22054140; PubMed=12059106;
RA      Mazarei M., Puthoff D.P., Hart J.K., Rodermel S.R., Baum T.J.;
RT      "Identification and characterization of a soybean ethylene-responsive
RT      element binding protein gene whose mRNA expression changes during
RT      soybean cyst nematode infection."
RL      Mol. Plant Microbe Interact. 15:577-586(2002).
DR      EMBL; AF537211; AAM45475.1; -
DR      HSSP; 080337; 2GCC.
DR      GO; GO:0005634; C:nucleus; IEA.
DR      GO; GO:0003700; P:transcription factor activity; IEA.
DR      GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR      InterPro; IPR000977; DNA_ligase.
DR      InterPro; IPR001471; TF_ERF.
DR      PRINTS; PR00367; ETHRSPELEMT.
DR      ProDom; PD001423; TF_ERF.1.
DR      SMART; SM00380; AP2; 1.
DR      PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
SQ      SEQUENCE 202 AA; 22467 MW; 1B875ACEB2A7D56D CRC64;

Query Match      9.4%; Score 19; DB 2; Length 202;
Best Local Similarity 100.0%; Pred.No. 1.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      79 GVRRRPWGKFAAETRDPKK 97
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RN      [3]
RP      SEQUENCE FROM N.A.
RA      Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA      Palm C.J., Bowser L., Jones T., Banh U., Carninci P., Chen H.,
RA      Cheuk R., Chung M.K., Hayaishizaki Y., Ishida J., Kamiya A., Kawai J.,
RA      Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA      Sakurai T., Satou M., Seki M., Shin P., Yamada K., Shinozaki K.,
RA      Ecker J., Theologis A., Davis R.W.;
RL      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RA      Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA      Palm C.J., Theologis A., Ecker J., Davis R.W.;
RL      Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RA      Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA      Palm C.J., Bowser L., Jones T., Banh U., Carninci P., Chen H.,
RA      Cheuk R., Chung M.K., Hayaishizaki Y., Ishida J., Kamiya A., Kawai J.,
RA      Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA      Sakurai T., Satou M., Seki M., Shin P., Yamada K., Shinozaki K.,
RA      Ecker J., Theologis A., Davis R.W.;
RL      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AC002388; AAC31840.1; -
DR      EMBL; AY072471; AAL66886.1; -
DR      EMBL; AF325089; AAK17157.1; -
DR      EMBL; AF370540; AAK48967.1; -
DR      PIR; T00409; T00409.
DR      HSSP; 080337; 2GCC.
DR      GO; GO:0005634; C:nucleus; IEA.
DR      GO; GO:0003700; P:transcription factor activity; IEA.
DR      GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR      InterPro; IPR000977; DNA_ligase.
DR      InterPro; IPR001471; TF_ERF.
DR      PRINTS; PR00367; ETHRSPELEMT.
DR      ProDom; PD001423; TF_ERF.1.
DR      SMART; SM00380; AP2; 1.
DR      PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
SQ      SEQUENCE 226 AA; 25353 MW; 4B2EF81CDD856987 CRC64;

Query Match      9.4%; Score 19; DB 2; Length 226;
Best Local Similarity 100.0%; Pred.No. 2.1e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      102 GVRRRPWGKFAAETRDPKK 120
Db      94 GVRRRPWGKFAAETRDPKK 112
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RA Feldmann K.;
RU Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY088387; AAM65925.1; -.
DR HSSP; 080337; 2GCC.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001471; TF_ERF.
DR PRINTS; PR00367; ETHRSP_ELMNT.
DR ProDom; PD001423; TF_ERF; 1.
DR SMART; SM00380; AP2; 1.
DR POSITIVE; PS00697; DNA_LIGASE_A1; UNKNOWN; 1.
SQ SEQUENCE 226 AA; 25367 MW; C3F80438CF19D80 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRRPWGKFAAIRDPK 120
Db 94 GVRRRPWGKFAAIRDPK 112

RESULT 5
O9LEM6 PRELIMINARY; PRT; 210 AA.
AC O9LEM6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AP2-domain DNA-binding protein.
GN Name=orca2;
OS Catharanthus roseus (rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Gentianales; Apocynaceae; Rauvolfioideae; Vincaceae;
OC Catharanthus.
OC NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G.don; TISSUE=Cell suspension;
RX MEDLINE=99380162; PubMed=10449411; DOI=10.1093/emboj/18.16.4455;
RA Menke F.L.H., Champion A., Kijne J.W., Memelink J.;
RT "A novel jasmonate- and elicitor-responsive element in the periwinkle
RT secondary metabolite biosynthetic gene Str interacts with a jasmonate-
RT and elicitor-inducible AP2-domain transcription factor, ORCA2."
RL EMBO J. 18:4455-4463(1999).
DR EMBL; AJ238740; CAB93940.1; -.
DR HSSP; 080337; 2GCC.
DR TRANSFAC; T04749; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001471; TF_ERF.
DR PRINTS; PR00367; ETHRSP_ELMNT.
DR ProDom; PD001423; TF_ERF; 1.
DR SMART; SM00380; AP2; 1.
DR DNA-binding.
SQ SEQUENCE 210 AA; 24021 MW; 017DF088F713CE38 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRRPWGKFAAIRDPK 119
Db 129 GVRRRPWGKFAAIRDPK 146

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AC Q7XD22;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative retrovirus-related pol polyprotein from transposon TNT.
GN ORFNames=OSJNBa0094K20.5;
OS Oryza sativa (Japanese cultivated rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RT "in-depth view of structure, activity, and evolution of rice
RT chromosome 10."
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RU Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017099; AAP5399.1; -.
DR HSSP; 080337; 1GCC.
DR Gramene; Q7XD22; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001471; TF_ERF.
DR ProDom; PD001423; TF_ERF; 1.
DR SMART; SM00380; AP2; 1.
DR Polyprotein.
KW POLYPROTEIN.
SQ SEQUENCE 124 AA; 13306 MW; CB857D9A551D81BE CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 9.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRRPWGKFAAIRDP 118
Db 15 GVRRRPWGKFAAIRDP 31

RESULT 7
Q6WK9 PRELIMINARY; PRT; 128 AA.
AC Q6WK9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE B1234D02.6 protein.
GN Name=B1234D02.6;
OS Oryza sativa (Japanese cultivated rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu Y., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Han B., Dai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA "Sequence and analysis of rice chromosome 4."
RL Nature 420:316-320(2002).
RN [2]
RP SEQUENCE FROM N.A.

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RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,  
RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,  
RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,  
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,  
RA Hao P., Zhang L., Mu M., Zhang R.O., Guan J.P., Fu G., Wang S.Y.,  
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,  
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,  
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,  
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.,  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BX842602; CAE5882.1; -;  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR001471; TF\_ERF.  
DR Pfam: PF00847; AP2; 1.  
DR PRINTS: PR00367; ETRSPLEEMNT.  
DR PRODOM: PD001423; TF\_ERF; 1.  
DR SMART: SM00380; AP2; 1.  
SQ SEQUENCE 128 AA; 14193 MW; 3BABAFPA81210A6 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 128;  
Best Local Similarity 100.0%; Pred. No. 9.8e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAEIRDP 118  
DB 14 GVRRRPWGKFAEIRDP 30

RESULT 8  
ID 09LTC5 PRELIMINARY; PRT; 139 AA.  
AC 09LTC5;  
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
DT 03-JUL-2004 (TREMBlrel. 27, last annotation update)  
DE Nicotiana glauca 3-like protein (Putative ethylene responsive element  
binding protein).  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsia.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20277480; PubMed=10819329;  
RA Nakamura Y.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
clones".  
RL DNA Res. 7:131-135(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.

RA Gong W., Pan Y., Peng X.Y., Yang J., Zhu Y.X.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB025608; BA95736.1; -;  
DR EMBL: AJ580377; CAE5639.1; -;  
DR HSSP: 080337; ZGCC.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR001471; TF\_ERF.  
DR PRINTS: PR00367; ETRSPLEEMNT.  
DR PRODOM: PD001423; TF\_ERF; 1.  
SQ SEQUENCE 139 AA; 16096 MW; 5E43AB05E93B4050 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 139;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 102 GVRRRPWGKFAEIRDP 118  
DB 22 GVRRRPWGKFAEIRDP 38

RESULT 9  
ID 075U5 PRELIMINARY; PRT; 165 AA.  
AC 075U5;  
DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)  
DE ERF-like protein.  
GN Name=CME-ERF;  
OS Cucumis melo (Muskmelon).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids I; Cucurbitales; Cucurbitaceae; Cucumis.  
OX NCBI\_TaxID=3656;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AB125975; BAD0155.1; -;  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR001471; TF\_ERF.  
DR Pfam: PF00847; AP2; 1.  
DR PRINTS: PR00367; ETRSPLEEMNT.  
DR PRODOM: PD001423; TF\_ERF; 1.  
DR SMART: SM00380; AP2; 1.  
SQ SEQUENCE 165 AA; 19063 MW; 0A829B3A53E0ADB9 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAEIRDP 118  
DB 85 GVRRRPWGKFAEIRDP 101

RESULT 10  
ID 08IDL4 PRELIMINARY; PRT; 201 AA.  
AC 08IDL4;  
DT 01-OCT-2002 (TREMBlrel. 22, last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)  
DE Ethylene responsive element binding factor-like.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsia.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22088475; PubMed=12093376;  
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,  
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
RT "Full-length messenger RNA sequences greatly improve genome  
annotation".  
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY085939; AAM63150.1; -;  
DR HSSP: 080337; ZGCC.

DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS; PR00367; ETRSPPELEMENT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SO SEQUENCE 201 AA; 22780 MW; 63511AF9BFBF0404 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAIRDP 118  
 DB 109 GVRRRPWGKFAAIRDP 125

## RESULT 11

084XB0 PRELIMINARY; PRT; 201 AA.  
 AC 084XB0;  
 DT 01-JUN-2003 (TReMBLrel. 24, Created)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Ethylene response factor 4.  
 GN Name=ERF4;  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Solanum.  
 NC NCB1\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=2816770; PubMed=12935902; DOI=10.1016/S0014-5793(03)00757-9;  
 RA Tournebise B., Sanchez-Ballester M.T., Jones B., Pesquet E., Regad F.,  
 RA Latche A., Pech J.C., Bouzayen M.;  
 RT "New members of the tomato ERF family show specific expression pattern  
 and diverse DNA-binding capacity to the GCC box element.";  
 RL FEBS Lett. 550:149-154(2003).  
 DR EMBL; AY192370; AA034706.1; -.  
 DR HSSP; O80337; 2GCC.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS; PR00367; ETRSPPELEMENT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SO SEQUENCE 201 AA; 22599 MW; 76075F3710881C90 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAIRDP 118  
 DB 121 GVRRRPWGKFAAIRDP 137

## RESULT 12

09FKG2 PRELIMINARY; PRT; 201 AA.  
 AC 09FKG2;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Transcription factor-like protein (putative ethylene responsive  
 element binding factor).  
 GN Name=At5g61590;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NC NCB1\_TaxID=3702;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=98403884; PubMed=9734815;  
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.  
 RT Sequence features of the regions of 1,367,185 bp covered by 19  
 RT Physically assigned P1 and P1C clones.";  
 RL DNA Res. 5:203-216(1998).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,  
 RA Carinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
 RA Seki M., Shim P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,  
 RA Theologis A.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]

RP SEQUENCE FROM N.A.  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J.M.,  
 RA Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,  
 RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,  
 RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB012239; BAB09003.1; -.  
 DR EMBL; AY045968; AAK76642.1; -.  
 DR EMBL; AY079321; AAL85052.1; -.  
 DR HSSP; O80337; 2GCC.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001471; TF\_ERF.  
 DR PRINTS; PR00367; ETRSPPELEMENT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SO SEQUENCE 201 AA; 22727 MW; 09BF68FB81696 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAIRDP 118  
 DB 109 GVRRRPWGKFAAIRDP 125

## RESULT 13

Q6V5F2 PRELIMINARY; PRT; 204 AA.  
 AC Q6V5F2;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE AP2 transcription factor.  
 GN CRFNames=Cr 7580;  
 OS Capsella rubella.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Capsella.  
 NC NCB1\_TaxID=81985;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SRRAIN=Circus maximus;  
 RX PubMed=14970339; DOI=10.1073/pnas.0305448101;  
 RA Flehig A., Kilmport R., Preuss D.;  
 RT "Comparisons of pollen coat genes across Brassicaceae species reveal  
 RT rapid evolution by repeat expansion and diversification.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:3286-3291(2004).  
 DR EMBL; AY350713; AAR15465.1; -.

DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; P:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR Pfam; PF00847; AP2; 1.  
 DR PRINTS; PR00367; ETHRSPELEMT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SQ SEQUENCE 204 AA; 23008 MW; E1D965603C9A4DCB CRC64;

Query Match 8.4%; Score 17; DB 2; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAEIRDP 118  
 |||||  
 DB 109 GVRRRPWGKFAAEIRDP 125

RESULT 14  
 Q6V5J8

PRELIMINARY; PRT; 206 AA.

AC Q6V5J8;  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DE AP2 transcription factor/ethylene response element.  
 GN ORFNames=Bo\_7580;  
 OS Brassica oleracea (Cauliflower).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3712;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A12BHD;  
 RX PubMed=14970339; DOI=10.1073/pnas.0305448101;  
 RA Flehig A., Kimport R., Preuss D.;  
 RT "Comparisons of pollen coat genes across Brassicaceae species reveal  
 RT rapid evolution by repeat expansion and diversification";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:3286-3291(2004).  
 DR EMBL; AY350710; ARL15499.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; P:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR Pfam; PF00847; AP2; 1.  
 DR PRINTS; PR00367; ETHRSPELEMT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SQ SEQUENCE 206 AA; 23288 MW; F7D0514D8B844CDA CRC64;

Query Match 8.4%; Score 17; DB 2; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAEIRDP 118  
 |||||  
 DB 112 GVRRRPWGKFAAEIRDP 128

RESULT 15

PRELIMINARY; PRT; 207 AA.

ID Q6V5B8;  
 AC Q6V5B8;  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DE AP2 transcription factor.  
 GN ORFNames=Aa1\_7580;  
 OS Arabidopsis arenosa.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=38785;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=care-1;  
 RX PubMed=14970339; DOI=10.1073/pnas.0305448101;  
 RA Flehig A., Kimport R., Preuss D.;  
 RT "Comparisons of pollen coat genes across Brassicaceae species reveal  
 RT rapid evolution by repeat expansion and diversification";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:3286-3291(2004).  
 DR EMBL; AY350715; ARL15499.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; P:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001471; TF\_ERF.  
 DR Pfam; PF00847; AP2; 1.  
 DR PRINTS; PR00367; ETHRSPELEMT.  
 DR ProDom; PD001423; TF\_ERF; 1.  
 DR SMART; SM00380; AP2; 1.  
 SQ SEQUENCE 207 AA; 23205 MW; EEAE49B874A1F282 CRC64;

Query Match 8.4%; Score 17; DB 2; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAEIRDP 118  
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 DB 112 GVRRRPWGKFAAEIRDP 128

Search completed: February 27, 2005, 22:26:24  
 Job time : 176 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 15:41:26 ; Search time 3857 Seconds  
(Without alignments)  
9949.840 Million cell updates/sec

Title: US-09-890-782-3

Sequence: 1 ttcttaaaaaagaagaaaaat.....ttatattcccaaaaagttcac 792

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_str: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792	100.0	792	6	BD269586 Method of
2	792	100.0	792	6	AX033192 Sequence
3	792	100.0	825	6	AX033192 Sequence
4	792	100.0	1816	6	CRO251249 Catharant
5	155.2	19.6	924	6	CRO251250 Catharant
6	135.6	17.1	914	8	CO808982 Sequence
7	134	16.9	681	8	AY088387 Arabidops
8	134	16.9	681	6	CO805290 Sequence
9	134	16.9	681	6	AX507520 Sequence
10	134	16.9	727	8	AF325089 Arabidops
11	134	16.9	841	8	AF072471 Arabidops
12	134	16.9	887	8	TOB8Y4A Arabidops
13	134	16.9	8534	8	AF370540 Arabidops
14	132.6	16.7	885	6	AC002388 Arabidops
15	132.6	16.7	885	6	BD269585 Sequence
16	132.6	16.7	905	6	AX033191 Sequence
17	131.4	16.6	703	8	CRO238740 Catharant
18	129.8	16.4	704	8	AF057373 Nicotiana
19	129.4	16.3	708	6	U89255 Lycopersico
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21	123.8	15.6	939	8	BT033151	BT033151	Lycopersi
22	122.2	15.4	931	8	AY192367	AY192367	Lycopersi
23	121.4	15.3	947	8	TOB8Y4D	TOB8Y4D	Nicotiana t
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26	116.2	14.7	933	6	AR432951	AR432951	Sequence
27	113.6	14.3	761	8	AF357211	AF357211	Glycine m
28	112.2	14.2	963	8	AY086983	AY086983	Arabidops
29	111.2	14.0	3688	8	AB016264	AB016264	Nicotiana
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31	110.6	14.0	732	6	AX412265	AX412265	Sequence
32	110.6	14.0	732	6	AX412465	AX412465	Sequence
33	110.6	14.0	732	6	AX412559	AX412559	Sequence
34	110.6	14.0	732	6	AX41895	AX41895	Sequence
35	110.6	14.0	732	6	AX505459	AX505459	Sequence
36	110.6	14.0	732	6	AX651319	AX651319	Sequence
37	110.6	14.0	908	8	AK175151	AK175151	Arabidops
38	110.6	14.0	913	6	AR439817	AR439817	Sequence
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#### ALIGNMENTS

RESULT 1  
BD269586  
LOCUS  
DEFINITION Method of modulating biosynthesis of metabolite in recombinant  
somatic cells.  
ACCESSION BD269586  
VERSION BD269586.1 GI:33079354  
KEYWORDS JP 2002535993-A/3.  
SOURCE Catharanthus roseus (Madagascar periwinkle)  
ORGANISM Catharanthus roseus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Gentianales; Apocynaceae; Rauvolfiaceae;  
Vincaceae; Catharanthus.  
1 (bases 1 to 792)  
Membelink,J., Der,C.T.B.V., Fits, Menke,F.L.H. and Kijne,J.W.  
METHOD Method of modulating biosynthesis of metabolite in recombinant  
somatic cells  
Patent: JP 2002535993-A 3 29-OCT-2002;  
RUKSUNIVERSITEIT LEIDEN  
OS Catharanthus roseus (madagascar periwinkle)  
PN JP 2002535993-A/3  
PD 29-OCT-2002  
PF 07-FEB-2000 JP 2000597442  
PR 05-FEB-1999 DK PA 199900158,10-FEB-1999 US 60/119388 PI  
JOHAN MEMELINK, CORNELIA THEODORA ELISABETH VAN DER FITS, PI  
FRANCISCUS LEONARDUS HENDRIKUS MENKE, JAN WILHEM KIJNE PC  
C12N15/09,A01H5/00,C12N5/10,C12P5/00,C12P7/22,C12P13/00,C12P17/ PC  
10, C12N15/00,C12N5/00  
PC Method of modulating biosynthesis of metabolite in recombinant  
somatic cells  
CC cells somatic  
CC Key Location/Qualifiers  
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FT Location/Qualifiers  
1..792  
/organism="Catharanthus roseus (madagascar periwinkle)"  
/mol\_type="genomic DNA"

## ORIGIN

/db\_xref="taxon:4058"

Query Match 100.0%; Score 792; DB 6; Length 792;  
Best Local Similarity 100.0%; Pred. No. 1.1e-205; Mismatches 0; Indels 0; Gaps 0;  
Matches 792; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 781 AAAAAAGTTGAC 792  
Db 781 AAAAAAGTTGAC 792

RESULT 2  
AX033192 AX033192 792 bp DNA linear PAT 21-SHP-2000  
LOCUS Sequence 3 from Patent WO046383.  
DEFINITION AX033192  
ACCESSION AX033192  
VERSION AX033192.1 GI:10280047  
KEYWORDS  
SOURCE Catharanthus roseus (Madagascar periwinkle)  
ORGANISM Catharanthus roseus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Gentianales; Apocynaceae; Rauvolfioideae;  
Vincaceae; Catharanthus.

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## ORIGIN

Query Match 100.0%; Score 792; DB 6; Length 792;  
Best Local Similarity 100.0%; Pred. No. 1.1e-205; Mismatches 0; Indels 0; Gaps 0;  
Matches 792; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 781 AAAAAGTTTCAC 792  
Db 781 AAAAAGTTTCAC 792

RESULT 3  
CRO251249 825 bp mRNA linear PLN 25-JUL-2000  
LOCUS Catharanthus roseus mRNA for AP2-domain DNA-binding protein (orca3 gene).  
DEFINITION

ACCESSION AJ251249  
VERSION AJ251249.1 GI:8980312  
KEYWORDS AP2-domain DNA-binding protein; orca3 gene.  
SOURCE Catharanthus roseus (Madagascar periwinkle)  
ORGANISM Catharanthus roseus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae; Catharanthus.

REFERENCE 1  
AUTHORS van der Fits,L. and Memelink,J.  
TITLE ORCA3, a jasmonate-responsive transcriptional regulator of plant primary and secondary metabolism  
JOURNAL Science 289 (5477), 295-297 (2000)  
MEDLINE 20355201  
PUBMED 10894776

REFERENCE 2 (bases 1 to 825)  
AUTHORS Memelink,J.  
TITLE Direct Submision  
JOURNAL Submitted (25-NOV-1999) Memelink J., Institute of Molecular Plant Sciences, Leiden University, Wassenaarseweg 64, NL-2333 AL, NETHERLANDS

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Query Match 100.0%; Score 792; DB 8; Length 825;  
Best Local Similarity 100.0%; Pred. No. 1.1e-205; Indels 0; Gaps 0;  
Matches 792; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 TCTACAGAGAAAATTGGAGAAATTTTTCGAGATTTTCTAAATTGGTGGAGATCCGAA 180

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QY 241 TGTTCAGAGAGATTCGTGTGGAGACCCGCGCAAGACGCGGCGCGGAGAGGTTGTCG 300  
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QY 781 AAAAAGTTTCAC 792  
Db 781 AAAAAGTTTCAC 792

RESULT 4  
CRO251250 1816 bp DNA linear PLN 25-JUL-2000  
LOCUS Catharanthus roseus orca3 gene for AP2-domain DNA-binding protein.  
DEFINITION  
ACCESSION AJ251250  
VERSION AJ251250.1 GI:8980314  
KEYWORDS AP2-domain DNA-binding protein; orca3 gene.  
SOURCE Catharanthus roseus (Madagascar periwinkle)  
ORGANISM Catharanthus roseus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae; Catharanthus.

REFERENCE 1  
AUTHORS van der Fits,L. and Memelink,J.  
TITLE ORCA3, a jasmonate-responsive transcriptional regulator of plant primary and secondary metabolism  
JOURNAL Science 289 (5477), 295-297 (2000)  
MEDLINE 20355201  
PUBMED 10894776

REFERENCE 2 (bases 1 to 1816)  
AUTHORS Memelink,J.  
TITLE Direct Submision  
JOURNAL Submitted (25-NOV-1999) Memelink J., Institute of Molecular Plant Sciences, Leiden University, Wassenaarseweg 64, NL-2333 AL,

NETHERLANDS									
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DB	1229 GATGACAGATTGGCTTATGATGACAGCGCGCTTAAATATGCGTGAAGCTAAAGCTT	1288							
QY	481 AATTTTCTCATTTGATTTGTTCCGAATTTTCCCGAACCCGTTAAGATTAACCCCGAGAAA	540							
DB	1289 AATTTTCTCATTTGATTTGTTCCGAATTTTCCCGAACCCGTTAAGATTAACCCCGAGAAA	1348							
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DB	1349 CGTTTCCGCGGAGACTTCTACAGACGTCGTCTTCTTCTTCTTCTTCTGCTGAAT	1408							
QY	601 AGTGAAGAGAGAGAGAGACGATATTAATTAATTAATTAAGTGAAGATTAAGAAAA	660							

Ddb	1409	AGTGAAGAGAAGAGAAGACGATTTAATTATTTATTTAAAGTGAAGATTTAAAAAA	1468
Qy	661	TTTCGTGAAGAAGATTTAATTAAGTGTGTTTTGTTAAACCCGATTAATCCCATTTGAA	720
Ddb	1469	TTCTGTGAAGAAGAGAATTAATTACGTGGTTTTTGTTAAAGCCCGATTAATCCCATTTGAA	1528
Qy	721	AATTATTAATCTTCATCATGTCCTTTTAAAACTTTGGAAATGTAACAAATTTTATATCC	780
Ddb	1529	AATTATTAATCTTCATCATGTCCTTTTAAAACTTTGGAAATGTAACAAATTTTATATCC	1588
Qy	781	AAAAAAGTTTAC 792	
Ddb	1589	AAAAAAGTTTAC 1600	
RESULT 5			
LOCUS	CQ808982	924 bp	DNA
DEFINITION	Sequence 285 from Patent WO2003097790.	linear	PAT 10-MAY-2004
ACCESSION	CQ808982		
VERSION	CQ808982.1	GI:47114376	
KEYWORDS			
SOURCE	Nicotiana tabacum (common tobacco)		
ORGANISM	Nicotiana tabacum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.		
AUTHORS	1. Inz,D.G., Goossens,A., Okeman-Caldentey,K.M., Haekinen,S.T. and Laakso,I.J.		
TITLE	Genes and uses thereof to modulate secondary metabolite biosynthesis		
JOURNAL	Patient: WO 2003097790-A 285 27-NOV-2003; Vlaams Internuiversiteitair Instituut voor Biotechnologie vzw w. (BE); VTT Biotechnology (FI)		
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Best Local Similarity	70.0%;	Pred. No. 3.2e-31;	
Matches 224;	Conservative 0;	Mismatches 93;	Indels 3; Gaps 1;
Qy	302	AGGATTGGACCGGATTAAGGCGTTTGAACGCGCGCGCGTGGGGAAGTTCCGCGCGGAGA	361
Ddb	370	AGGATTGGACCGGATTAAGGCGTTTGAACGCGCGCGCGTGGGGAAGTTTCCGCGGAGA	429
Qy	362	TAAAGGATCCGAAAAAGAAAGATCCAGATTTGTTGGGTTCATACGAGACACTCTGAG	421
Ddb	430	TAAAGGATCCGAGAGAAAGAGCGCGAGATTATGCTTAGGAACTTACAGAGCCAGAGG	489
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Ddb	490	AGCGACGATTGGCTTATGATGACGCGCGTTTCAAAATCCGCGGCTCGAAGCTCGGCTCA	549
Qy	482	ATTTTCCTCATTTGATTGTTCCGAATTTCCGGAACCGTTAGAGTAAACCCGAGAAAC	541
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Ddb	607	GTACCGCTTACGCGCTCACCCAGCGATGCTCTTCTTCACTATCATCATCATAGAAATG	666
Qy	602	GTGAGAGAAAGAGAAGAGA 621	
Ddb	667	GGACAAGAAAAAGAAAAATA 686	
RESULT 6			



AY088387  
LOCUS AY088387 914 bp mRNA linear PLN 14-APR-2003  
DEFINITION Arabidopsis thaliana clone 6397 mRNA, complete sequence.  
ACCESSION AY088387  
VERSION AY088387.1 GI:21407161  
KEYWORDS FLI CDNA.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
AUTHORS Haas, B.J., Volkovskiy, N., Town, C.D., Torkhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.  
TITLE Full-length messenger RNA sequences greatly improve genome annotation  
JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)  
MEDLINE 22088475  
PUBMED 12093376  
REFERENCE  
AUTHORS Brover, V., Torkhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.  
TITLE Full-length cDNA from Arabidopsis thaliana  
JOURNAL Unpublished  
AUTHORS Brover, V., Torkhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.  
TITLE Direct Submission  
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA  
COMMENT  
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or later ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Geneset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.  
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Best Local Similarity 64.2%; Pred. No. 7,66-26;  
Matches 204; Conservative 0; Mismatches 114; Indels 0; Gaps 0;  
QY 233 CGAAGAGCTGTCAAGAGATTCTGTTGGGAAACCCCGCAGAGCGCGCGAGAG 292  
Db 290 CCGTACCTCTCCGCGAGAGATAAGCTCCGCGAGAGCGAGCGAGTGCACACG 349

QY 293 GTTGTTCAGAGATTGGAAACCGGTATTAAGGCGCTTAGACGCGCGCGGAGGAGTTCC 352  
Db 350 CGCGGAGCGAGAGAGGAGATGCACTACAGAGATGAGAGAGCCGTGGGAAATTCC 409  
QY 353 CGCGGAGATTAAGGATTCGAAAAGAAAGATCCAGATTTGGTGTACATACAGA 412  
Db 410 CGCGGAGATTAGGATTCGAAAGAAAGACGAGCTAGGGTTTGGCTCGGACCTTACGAGA 469  
QY 413 CACCTAGAGATGACGATTTGGCTTATGATGACAGCCCGCTTATATGCGTGAGCTTAAG 472  
Db 470 CGCGGAGAGCGCGGCGTGGCTTACGACCGAGCGCGCTTTCAGCTCAGAGATCGAAG 529  
QY 473 CTAGGCTTATTTCTCATTTGATTTGTTGCAATATTTCCGACCGGTAGAGTAAC 532  
Db 530 CTAGCTGAATTTTCCGCAATTTGATTTGTTTCTTGTAGATGAGCCGTTAGATTAAGC 589  
QY 533 CGAAGAAACGTTTCCCTG 550  
Db 590 CTCGCGTGGCTGCGCGG 607  
RESULT 7  
LOCUS CO805290 681 bp DNA linear PAT 10-MAY-2004  
DEFINITION Sequence 1701 from Patent WO2004035798.  
ACCESSION CO805290  
VERSION CO805290.1 GI:47111279  
KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
AUTHORS Inze, D., de Veylder, L. and Vlieghe, K.  
TITLE Identification of novel e2f target genes and use thereof  
JOURNAL Patent: WO 2004035798-A 1701 23-APR-2004; Cropdesign N.V. (BE)  
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Best Local Similarity 63.8%; Pred. No. 2e-25;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;  
QY 233 CGAAGAGCTGTCAAGAGATTCTGTTGGGAAACCCCGCAGAGCGCGCGAGAG 292  
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QY 293 GTTGTTCAGAGATTGGAAACCGGTATTAAGGCGCTTAGACGCGCGCGGAGGAGTTCC 352  
Db 251 CGCGGAGCGAGAGAGGAGATGCACTACAGAGATGAGAGAGCCGTGGGAAATTCC 310  
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Db 311 CGCGGAGATTAGGATTCGAAAGAAAGACGAGCTAGGGTTTGGCTCGGACCTTACGAGA 370  
QY 413 CACCTAGAGATGACGATTTGGCTTATGATGACAGCCCGCTTATATGCGTGAGCTTAAG 472  
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RESULT 8  
AX507520 681 bp DNA linear PAT 27-SEP-2002  
LOCUS Sequence 2215 from Patent WO0216655.  
DEFINITION AX507520  
ACCESSION AX507520 GI:23388757  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Harper, J.F., Kreps, J., Wang, X. and Zhu, T.  
Stress-regulated genes of plants, transgenic plants containing  
same, and methods of use  
Patent: WO 0216655-A 2215 28-FEB-2002;  
The Scripps Research Institute (US); Syngenta Participations AG  
(CH)  
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QY 233 CGGAAGCTGTGAGAGATTCTGTGTGGAACCCCGCAGAGCGCGCGAGAG 292  
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JOURNAL  
Submitted (30-NOV-2000) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA  
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source  
Location/Qualifiers  
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QY 233 CGGAAGCTGTGAGAGATTCTGTGTGGAACCCCGCAGAGCGCGCGAGAG 292  
DB 191 CGCTTACCTCTCCGGGAGGAAATTAAGCTCCGCGAGAGAGAGTGCCTACACG 250  
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DB 311 CGCGGAGATTAAGGATTCGAAAGAGAGATTCGATTTGTTGGTATCATACGAGA 370  
QY 413 CACCTGAGATGAGCATTTGCTTATGATGACCGCGCTTATATGCTGAGCTAAAG 472  
DB 371 CGCGGAGAGAGCGCGGCTGCTGCTACAGCGCGCGCTTACAGCTCAGAGATGAGAG 430  
QY 473 CTAGGCTTAATTTCTCATTTGATTTGTTGAAATATTTCCGAGCCCGTTAGATTAAC 532  
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RESULT 10  
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LOCUS AY072471  
DEFINITION Arabidopsis thaliana putative ethylene response element binding  
protein (EREBP) (At2g44840; T13F1.15) mRNA, complete cds.  
ACCESSION AY072471  
VERSION AY072471 GI:18377439  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Arabidopsids thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
1 (bases 1 to 727)  
REFERENCE  
AUTHORS  
Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M.,  
Palm, C.J., Chung, L., Jones, T., Barn, J., Carrinci, P., Chen, H.,  
Cheuk, R., Bowers, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A.,  
Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Nam, P.K.,  
Sakano, H., Sakurai, T., Satou, M., Seki, M., Shim, P., Yamada, K.,

TITLE  
Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.

JOURNAL  
Submitted (02-JAN-2002) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA

COMMENT  
e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN  
Arabidopsis Full-length cDNA'): Seki, M., Natsumasa, M., Ishida, J.,  
Sato, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,  
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the  
sequencing and annotation of the RAFL cDNAs: Nguyen, M.,  
Soutwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C. J.,  
Bower, L., Jones, J., Bann, J., Chen, H., Cheuk, R., Chung, M. K.,  
Kim, C., Lin, J., Liu, S. X., Pham, P. K., Sakano, H., Shim, P.,  
Yamada, K., Ecker, J., Theologis, A. and Davis, R. W.

Nguyen, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed  
equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R. W.  
(SSP/Stanford) contributed equally to this work as PIs.

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## ORIGIN

Query Match 16.9%; Score 134; DB 8; Length 727;  
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Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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Db 491 CTCGCCGTGCTGCGCG 508

RESULT 11

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LOCUS  
DEFINITION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Nicotiana tabacum mRNA for ERF1, complete cds.  
D38123.1 GI:790359  
ERF1, ethylene-responsive transcription factor.  
Nicotiana tabacum (common tobacco)  
Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Nicotiana.

REFERENCE  
AUTHORS  
TITLE  
Ohme-Takagi, M. and Shinozaki, H.  
Ethylene-inducible DNA binding proteins that interact with an  
ethylene-responsive element  
Plant Cell 7 (2), 173-182 (1995)

JOURNAL  
MEDLINE  
PUBMED  
7756828  
55276459

REFERENCE  
AUTHORS  
TITLE  
Suzuki, K., Suzuki, N., Ohme-Takagi, M. and Shinozaki, H.  
Immediate early induction of mRNAs for ethylene-responsive  
transcription factors in tobacco leaf strips after cutting  
Plant J. 15, 657-665 (1998)

JOURNAL  
TITLE  
Submitted (01-SEP-1994) Masaru Ohme-Takagi, National Institute of  
Bioscience and Human Technology, Plant Molecular Biology  
Laboratory, 1-1 Higashi, Tsukuba, Ibaraki 305, Japan  
(E-mail:masaru@nih.go.jp, Tel:0298-54-6071, Fax:0298-54-6095)  
Sequence updated (04-Apr-1995) by:  
Masaru Ohme-Takagi.

## COMMENT

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source  
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## 5'UTR

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Query Match 16.9%; Score 134; DB 8; Length 841;  
Best Local Similarity 59.0%; Pred. No. 2e-25;  
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288 AGGAGTTGTTCAAGAGATTGGAACCGGTAAAGGCGCTTACGCGCGCGCGGAGAA 347

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Db	374	ATTTCGCCGCGGAGATTAGGAGATCCGGCGAAAATGAGACTAGGGTTTTGGTGAAACATA	433
OY	408	CGAGACACCTAGAGATGAGCATGGCGCTTATGATGACACCGCGTTTAATATGCGTGGAGC	467
Db	434	CGAAACAGATGAGAAGCTGCATTGCTTATGATTAACCGGCTTATATAAATGCGGGTTC	493
OY	468	TAAAGCTAGCTATATTTTCCATATTGATTTGTCGAATATTTTCGGACCCTTAGAGT	527
Db	494	AAAGGCTATTTAATATTTTCCACANAGATGGTTTAATATGAACCGGAACGGTTCCAGT	553
OY	528	AAACCCGAGAAAACGTTTCCCTCGGAGCCCTTTACAGCGTCGTCGTCCTTCTTCTTC	587
Db	554	TACGCGCAAAAAGACAGCAGCATCGCCCTGAACCGGCTAGTTCCTCGMAAATAGTCACTAA	613
OY	588	TTGCTGTGAATAATAGTGAGGAGAGAA	617
Db	614	ACGGAGAAAGAAAGCGCTGTTGCAACTGAGAA	643
RESULT 12			
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LOCUS DEFINITION	Arabidopsis thaliana putative ethylene response element binding protein; EREBP [At2g44840; T1JEL5.15] mRNA, complete cds.		
ACCESSION	AF370540		
VERSION	AF370540.1 GI:13899090		
KEYWORDS	FLI CDNA.		
SOURCE ORGANISM	Arabidopsis thaliana (chale cress)		
REFERENCE	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi. 1 (bases 1 to 887)		
AUTHORS	Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,U., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shim,P., Yamada,K., Shinozaki,K., Eckert,J., Theologis,A. and Davis,R.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-Apr-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA		
COMMENT	e-mail for correspondence: ardb@sequence.stanford.edu		
	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arbidopsis Full-length cDNA': Seki,M., Narusaka,M., Ishida,U., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.		
	The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shim,P., Yamada,K., Eckert,J., Theologis,A. and Davis,R.W.		
	Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.		
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LOCUS		
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VERSION	AC002388.3	
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ORGANISM	Arabidopsis thaliana (thale cress)	
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REFERENCE	1 (bases 1 to 85534) Ketchum,K.A., Crosby,M.L., Brandon,R.C., Rounsley,S.D., Lin,X., Kerlavage,A.R., Adams,M.D., Somerville,C.R. and Venter,D.C.	
AUTHORS	Unpublished	
JOURNAL	2 (bases 1 to 85534)	
REFERENCE	LIn.X.	
AUTHORS	Direct Submission	
TITLE	Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA	
JOURNAL	3 (bases 1 to 85534)	
REFERENCE	Town,C.D. and Kaul,S.	
AUTHORS	Direct Submission	
TITLE	Submitted (27-FEB-2002) The Institute for Genomic Research, 9712	
JOURNAL		

Medical Center Dr, Rockville, MD 20850, USA, cdtown@igr.org  
On Apr 18, 2002 this sequence version replaced gi:6598367.  
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 VERSION BD269585.1 GI:33079933  
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Gentianales; Apocynaceae; Rauvolfioideae;  
 Vincaceae; Catharanthus.

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REFERENCE 1 (bases 1 to 885)
AUTHORS Memelink,J., Der,C.T.E.V., Pits, Wenke,F.L.H. and Kijne,J.W.
TITLE Method of modulating biosynthesis of metabolite in recombinant
JOURNAL somatic cells
COMMENT Patent: JP 2002535993-A 2 29-OCT-2002;
RUKUNIVERSITEIT LEIDEN
O6 Catharanthus roseus (madagascar periwinkle)
PN JP 2002535993-A/2
PD 29-OCT-2002
PF 07-FEB-2000 JP 2000597442
PR 05-FEB-1999 DK PA 199900158, 10-FEB-1999 US 60/119388 PI
Johan Memelink, Cornelia Theodora Elisabeth van der Pits, Pi
Franciscus Leonardus Hendrikus Menke, Jan Willems Kijne PC
C12N15/09,A01H5/00,C12N5/10,C12P5/00,C12B7/22,C12P13/00,C12P17/
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 ORGANISM  
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 asterids; lamids; Gentianales; Apocynaceae; Rauvolfioideae;  
 Vincaceae; Catharanthus.  
 REFERENCE 1  
 Memelink,J., Kijne,J.W., Menke,F.L. and van der Pits,C.T.  
 AUTHORS Memelink,J., Kijne,J.W., Menke,F.L. and van der Pits,C.T.  
 TITLE Method of modulating metabolite biosynthesis in recombinant cells  
 JOURNAL Patent: WO 0046383-A 2 10-AUG-2000;

UNIV LEIDEN (NL) ; MEMELINK JOHAN (NL) ; FITS CORNELIA THEODORA  
ELISABE (NL) ; KIJNE JAN WILLEM (NL) ; MENKE FRANK LEONARDUS  
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Location/Qualifiers

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PS Disclosure, Page 95; 101pp; English.

XX Many plant secondary metabolites have value as pharmaceuticals, food  
CC colourings, flavours and fragrances. Some plant secondary metabolites are  
CC linked to plant or plant cell defence mechanisms and may confer to the  
CC plant antimicrobial activity, protection against UV light, herbivores,  
CC pathogens, insects and nematodes. Plant secondary metabolites such as  
CC terpenoid, indole alkaloids (TIA) represent a class of pharmaceutically  
CC useful compounds which naturally occur in many plant species. New methods  
CC are described which modulate the expression of one or more genes involved  
CC in the biosynthesis of plant metabolites or their precursors in plant  
CC cells. The method comprises inserting into a plant cell a sequence  
CC encoding a transcription factor comprising an AP2 DNA-binding domain and  
CC by modifying the expression of that transcription factor. Transcription  
CC factors comprising an AP2 DNA-binding domain are useful as central  
CC regulators of complex metabolic pathways involving numerous target genes  
CC for such transcription factors. This means that the yield of commercially  
CC valuable metabolite compounds can be enhanced and the tolerance of plants  
CC towards exogenous stress factors can be influenced. The method is useful  
CC for modulating the level of one or more metabolites. By providing a  
CC transcription factor to the cell the level of the metabolite is enhanced  
CC by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to  
CC a cell to which the transcription factor is not provided  
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DB 601 AGTGAAGAAAGAAAGAGACGATTAATTAATTAATTAATTAATTAATTAATTAATTA 660

QY 661 TTTGTGAATGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 720  
DB 661 TTTGTGAATGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 720  
QY 721 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 780  
DB 721 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 780  
QY 781 AAAAAGTTGAC 792  
DB 781 AAAAAGTTGAC 792

# RESULT 2

ADP9769 standard; cDNA; 924 BP.

ADP9769;

26-FEB-2004 (first entry)

Nicotiana tabacum variant bright yellow nucleotide sequence SEQ ID:285.

secondary metabolite modulator; biosynthesis; alkaloid; phenylpropanoid;

tabacco; Nicotiana tabacum variant bright yellow; Nicotiana tabacum BY;

plant; gene; ss.

Nicotiana tabacum.

MO2003097790-A2.

16-MAY-2003; 2003MO-BP050171.

17-MAY-2002; 2002EP-00076973.

04-JUL-2002; 2002EP-0007674.

(VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

(VLTB-) VTT BIOTECHNOLOGY.

Inze DG, Goossens A, Oksman-Caldentey K, Haekinen ST, Laakso JU;

WPI; 2004-022853/02.

New isolated polypeptides and polynucleotides useful for modulating the

biosynthesis of secondary metabolites (e.g. alkaloids or

phenylpropanoids) in an organism or its cell.

Claim 3; SEQ ID NO 285; 140pp; English.

The present invention describes an isolated polypeptide that modulates

the production of at least one secondary metabolite in an organism, or

its derived cell. The polypeptide is selected from a polypeptide encoded

by a polynucleotide comprising any of the 871 nucleotide sequences given

in the specification. The polypeptides and polynucleotides are useful in

modulating the biosynthesis of secondary metabolites (e.g. alkaloids or

phenylpropanoids) in an organism or its derived cell. The present

sequence is used in the exemplification of the present invention.

Sequence 924 BP; 309 A; 188 C; 189 G; 238 T; 0 U; 0 Other;

Query Match 19.6%; Score 155.2; DB 12; Length 924;

Best Local Similarity 70.0%; Pred. No. 9e-32;

Matches 224; Conservative 0; Mismatches 93; Indels 3; Gaps 1;

QY 302 AGATTGAAACCGGTATTAAGGCGGCTTGAACGCGCGCGTGGGGAAGTTCCGCGCGGAGA 361

DB 370 AAGATTGGAACCGGTATTAAGGCGGCGCGCGTGGGGAAGTTTTCGCGCGAGA 429

QY 362 TAAGGATCCGAAAGAAAGAGATCCAGATTTGGTGGTACATACGACACCTGAGG 421

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Qy      422 ATGCACATTGGCTTATGATGACGCCGCTTAAATATGCTGAGCTAAAGCTTAGCTTA 481
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Qy      482 ATTTTCTCATTTGATTGTTGCAATATTTCCGAGCCCGTTAGATAACCCGAGAAAC 541
Db      550 ATTTTCTCATTTATTTGATCAAACTTTCTTAAGCCGCTAGATTACAGCAAG--AC 606
Qy      542 GTTTCCTCGGAGACCTTCTACGACGTCGTCTTCTTCTTCTTCTTCTTCTGAAATA 601
Db      607 GTAGCGGTACGGCGCTACCCGACCATCGTCTTCTTATCTATCTATCAGAAATG 666
Qy      602 GTGAGAGAAAGAAAGAGA 621
Db      667 GGCACAGAAAAAGAAATA 686

RESULT 3
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ID      AAC40522 standard; DNA; 914 BP.
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AC      AAC40522;
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DT      17-OCT-2000 (first entry)
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DE      Arabidopsis thaliana DNA fragment SEQ ID NO: 28610.
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KW      Hybridization assay; genetic mapping; gene expression control;
KW      protein identification; signal transduction pathway; metabolic pathway;
KW      promoter; termination sequence; ss.
XX
OS      Arabidopsis thaliana.
XX
PN      EP1033405-A2.
XX
PD      06-SEP-2000.
XX
PF      25-FEB-2000; 2000EP-00301439.
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Query Match 17.1%; Score 135.6; DB 3; Length 914;  
Best Local Similarity 64.2%; Pred. No. 2e-26;  
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DB 290 CCGTTACCTCTCCGGCGGAGGAAGATTAAGCTCCGGCGAGAAAGCGATGCTCACACG 349  
QY 293 GTTGTTCGAAGATTGGAACCGGTATTAAGCGCGCTTGAACGCGCGCTTGGGGAAGTTG 352  
DB 350 CGCCGAGGAGAAAGGAGATGCAATACAGAGAGTGAAGGAGGCGCTGGGGAATTCG 409  
QY 353 CGGCGAGATTAAGGATCCGAAAGAAAGATCCAGATTTGGTTGGTACATACAGA 412  
DB 410 CGGCGAGATTAAGGATCCGAAAGAAAGATCCAGATTTGGTTGGTACATACAGA 469  
QY 413 CACCTGAGATGAGCATTTGCTTATGATGACGCGCTTTAATATGCGTAGCTAAG 472  
DB 470 CGCGGAGAGACGCGCGGTGGGTACGACGAGCGCGCTTTCAGCTCAGAGATCGAAG 529  
QY 473 CTAGGCTTAATTTTCTCTCATTTGATTGTTCCGAATATTTCCGAGCCGCTTAAGTAAC 532  
DB 530 CTAGGCTGAATTTCCGCAATTGATTGTTCTGTATGATGAGCGCGTAGAATTAGGC 589  
QY 533 CGAGAAAGCTTCCCTG 550  
DB 590 CTCGCCGTCCCTCCCG 607  
  
RESULT 4  
ID ABZ14410 standard; DNA; 681 BP.  
XX ABZ14410;  
AC ABZ14410;  
XX 21-JAN-2003 (first entry)  
DT  
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2215.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2215.  
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
KW Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
XX W0200216655-A2.  
PN W0200216655-A2.  
XX 28-FEB-2002.  
PD 28-FEB-2002.  
XX 24-AUG-2001; 2001MO-US026685.  
PF 24-AUG-2001; 2000US-0227866P.  
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PR 26-JAN-2001; 2001US-0264647P.  
PR 22-JUN-2001; 2001US-0300111P.  
XX (SGRI ) SCRIIPS RES INST.  
PA (SYGN ) SYNGENRA PARTICIPATIONS AG.  
XX Harper JF, Kreps J, Wang X, Zhu T;  
XX WPI; 2002-304127/34.  
DR WPI; 2002-304127/34.  
XX Identifying a stress condition to which a plant cell has been exposed and  
FT producing plants with increased tolerance to these abiotic stresses.  
XX  
PS Claim 144; SEQ ID NO 2215; 577bp + Sequence Listing; English.  
CC The invention relates to identifying a stress condition to which a plant  
CC cell has been exposed, comprising: (a) contacting nucleic acid  
CC representative of expressed polynucleotides in the plant cell with an  
CC array or probes representative of the plant cell genome; and (b)  
CC detecting a profile of expressed polynucleotides in the plant cell



PD 16-MAY-2002.  
XX 26-JAN-2001; 2001US-00770149.  
XX 27-JAN-2000; 2000US-0178506P.  
XX (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
XX Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;  
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;  
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;  
PI Hurban P;  
XX WPI; 2002-479224/51.  
XX New nucleic acid that hybridizes to Arabidopsis thaliana sequences,  
PT useful e.g. for preparing transgenic plants with increased resistance or  
XX altered metabolism.  
XX Claim 1; SEQ ID NO 325; 40bp + Sequence Listing; English.  
XX The invention relates to nucleic acids (I) that hybridise under stringent  
CC conditions to any of 999 sequences (AB065424-AB066422) or their  
CC fragments. (I) are used to express the corresponding polypeptides (II) or  
CC to produce genetically modified plant cells or transgenic plants, which  
CC may have improved resistance to disease or stress, or altered  
CC metabolic/biosynthetic pathways (for production of commercial,  
CC nutritional or medicinal products), or generally any trait of interest,  
CC or can be used to screen for biologically active agents (e.g. fungicides,  
CC insecticides and antibiotics). Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from the USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=99909770149  
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SQ Sequence 685 BP; 171 A; 139 C; 202 G; 173 T; 0 U; 0 Other;  
Query Match 16.9%; Score 134; DB 6; Length 685;  
Best Local Similarity 63.8%; Pred. No. 4.8e-26;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;  
QY 233 CGGAAAGCTGTCAAGAGATTCTGTGTGGAAACCCCGCAGAACCGCGCGGAGAG 292  
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DB 193 CGCGGAGATTAGGATCCAGAAAGAACGAGAGTGAAGGTTTGGCTCGGACTTACGAGA 252  
QY 413 CACCTGAGATGACGATGGCTTATGATGATCAGCCGCTTAAATATCGGTGAGACTTAAG 472  
DB 253 CGCGGAGGAGCGCGCGGTGGCTTACGACCGAGCGGCGTTTCAAGTCAAGAGATCCGAAG 312

QY 473 CTAGGCTTAATTTCTCTCATTTGATTGTTCCGAATATTTCCGAGCCGTTAGAGTAAACC 532  
DB 313 CTBAGCTGAATTTTCGAGATTGATTGTTCTTGAAGATATAGCCGTTAGATTAAGGC 372  
QY 533 CGAGAAACGTTTCCCTG 550  
DB 373 CTCGCCGTGCTGCCGG 390  
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XX 18-OCT-2000 (first entry)  
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XX Arabidopsis thaliana DNA fragment SEQ ID NO: 42374.  
DE  
XX Hybridisation assay; genetic mapping; gene expression control;  
XX protein identification; signal transduction pathway; metabolic pathway;  
XX promoter; termination sequence; ss.  
OS Arabidopsis thaliana.  
XX  
XX EP1033405-A2.  
PN  
PD 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-00301439.  
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XX 25-FEB-1999; 99US-0121825P.  
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PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
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PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
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PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147993P.

PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150586P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157853P.  
PR 06-OCT-1999; 99US-0157853P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 22-OCT-1999; 99US-0161040P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 25-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 26-OCT-1999; 99US-0161200P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 16.9%; Score 134; DB 3; Length 781;

Best Local Similarity 63.8%; Pred. No. 5e-26;

Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 233 CGGAAGCTGTGAGGAGATTCTGTGTGGAACCCCGCAGAGCGCGCGGAGAG 292

Db 291 CCGTTACTCTCCGCGGAGGAAAAATAGCTTCGCGGACGAGGCGAGTGCGTCAACG 350  
Qy 293 GTTGTTCGAGGATTTGAACCCGTTATTAAGGCGGTTAGACGCGCGCGCTGGGGAAATTTCG 352  
Db 351 CCGCGAGGAGAGAGGAGATGACGTACAGAGAGTAGAGAGAGCGCGCTGGGGAAATTTCG 410  
Qy 353 CCGCGAGATTAAGGATCCGAAAAAGAAAGATCCAGATTTGGTTGGTACATTCGAGA 412  
Db 411 CCGCGAGATTAAGGATCCGAAAAAGAAAGATTAAGGATTTGGCTCGGGAATTACAGA 470  
Qy 413 CACCTGAGATGAGATTTGGCTTATGATGACGCGCGCTTATATGCGTGAAGTAAAG 472  
Db 471 CCGCGAGGACGCGGCGGTGCGTACGACGAGCGCGCTTCACTCAGAGGATGAAAG 530  
Qy 473 CTAGGCTTAATTTCTCCTCATTTGATTGTTCCGAAATATTTCCGAGCCGTTAGAGTAAAC 532  
Db 531 CTAAAGTGAATTTTCGCGATTTGATTGTTCTTGTAGATGAGCGGTTAGATTAAGC 590  
Qy 533 CGAGAAACGTTTCCCTG 550  
Db 591 CTCGCGCTGCTGCGCGG 608

RESULT 8  
AAD06444 standard; cDNA; 913 BP.  
ID AAD06444;  
AC AAD06444;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
XX Arabidopsis thaliana transcription factor G22 cDNA.  
DE Transcription factor; environmental stress tolerance; gene therapy;  
KM plant structure; plant development; ss.  
XX Arabidopsis thaliana.  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 81..761  
FT /tag= a  
FT /product= "Arabidopsis thaliana transcription factor"  
XX  
PN W0200136598-A1.  
XX  
PD 25-MAY-2001.  
XX  
PF 14-NOV-2000; 2000MO-US031458.  
XX  
PR 17-NOV-1999; 99US-0166228P.  
PR 17-APR-2000; 2000US-0197899P.  
PR 22-AUG-2000; 2000US-0227439P.  
XX  
XX (MEND-) MENDEL BIOTECHNOLOGY INC.  
PA (PINE/) PINEDA O.  
PA (YUG/) YU G.  
PA (CREE/) CREELMAN R.  
PA (RIEC/) RIECHMANN J L.  
PA (HEAR/) HEARD J.  
PA (RATC/) RATCLIFFE O.  
PA (REUB/) REUBER L.  
PA (KEDD/) KEDDIE J.  
XX  
PI Pineda O, Yu G, Creelman R, Riechmann JL, Heard J, Ratcliffe O;  
PI Reuber L, Keddie J;  
XX  
XX WPI; 2001-336000/35.  
DR P-PSDB; AAE02464.  
XX  
XX Nucleic acids encoding plant transcription factor polypeptides, useful  
PT for altering the environmental stress tolerance characteristics of  
PT plants.  
XX

PS Claim 4; Page 54-55; 116pp; English.  
XX  
XX The present sequence is a cDNA encoding Arabidopsis thaliana  
CC transcription factor. This novel transcription factor is useful for  
CC modifying a plant's phenotype in desirable ways, such as modifying a  
CC plant's environmental stress. The transcription factor is encoded by  
CC environmental stress tolerance gene derived from Arabidopsis thaliana.  
CC The transcription factors and the genes encoding them are used to alter  
CC the structure and developmental characteristics of plants such as  
CC soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower,  
CC alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry,  
CC raspberry, cantaloupe, carrot, cauliflower, coffee, onion, cucumber,  
CC eggplant, grapes, honey dew, lettuce, mango, melon, papaya, pea,  
CC peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato.  
CC watermelon, roseaceous fruits and/or vegetable brassicas. These sequences  
CC are also used for modifying traits associated with environmental stresses  
CC tolerance, such as freezing, chilling, heat, drought, water saturation,  
CC salt, photoconditons, radiation and ozone. The transcription factors are  
CC used in gene therapy  
XX  
XX Sequence 913 BP; 249 A; 190 C; 236 G; 238 T; 0 U; 0 Other;

Query Match 16.9%; Score 134; DB 4; Length 913;  
Best Local Similarity 63.8%; Pred. No. 5.4e-26;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 233 CCGAAAGCTGTACAGAGATTTCTGTGTGGAAACCCGCGAGAGCGCGCGAGAG 292  
Db 271 CCGTTACTCTCCGCGGAGGAAAAATAGCTTCGCGGACGAGAGGATGCTCAACG 330  
Qy 293 GTTGTTCGAGGATTTGAACCCGTTATTAAGGCGGTTAGACGCGCGCTGGGGAAATTTCG 352  
Db 331 CCGCGAGGCGAGAGGAGATGAGTACAGAGAGTGGAGGAGCGCGCTGGGGAAATTTCG 390  
Qy 353 CCGCGAGATTAAGGATTCGAAAAAGAAAGATCCAGATTTGGTTGGTATCATTCGAGA 412  
Db 391 CCGCGAGATTAAGGATTCGAAAAAGAAAGATCCAGATTTGGTTGGTATCATTCGAGA 450  
Qy 413 CACCTGAGATGAGATTTGGCTTATGATGACGCGCGCTTATATGCGTGAAGTAAAG 472  
Db 451 CCGCGAGAGCGCGCGGTGCGTACGACCGAGCGCGCTTCACTCAGAGGATGAAAG 510  
Qy 473 CTAGGCTTAATTTCTCCTCATTTGATTGTTCCGAAATATTTCCGAGCCGTTAGAGTAAAC 532  
Db 511 CTAAAGTGAATTTTCGCGATTTGATTGTTCTTGTAGATGAGCGGTTAGATTAAGC 570  
Qy 533 CGAGAAACGTTTCCCTG 550  
Db 571 CTCGCGCTGCTGCGCGG 588

RESULT 9  
ADE37188 standard; cDNA; 913 BP.  
ID ADE37188;  
XX  
AC ADE37188;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
XX Plant yield related polynucleotide clone G22.  
DE  
XX  
XX dsf gene; transcription factor; tolerance; environmental condition;  
KM microbial disease; fungal disease; viral disease; pest infestation;  
KM herbicide sensitivity; heavy metal tolerance; heavy metal uptake;  
KM growth improvement; photocondition; nutrient uptake; hormone sensitivity;  
KM transgenic plant.  
XX Arabidopsis thaliana.  
OS  
XX  
XX Key Location/Qualifiers  
FT CDS 81..761  
FT /tag= a  
FT /product= "transcription factor"  
FT



```
XX MO2003014327-A2.
PN
XX
XX PD
XX 20-FEB-2003.
PF
XX 09-AUG-2002; 2002WO-US026966.
XX
XX 09-AUG-2001; 2001US-0310847P.
PR 19-NOV-2001; 2001US-0336049P.
PR 11-DEC-2001; 2001US-0338692P.
PR 14-JUN-2002; 2002US-00171468.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
PI Reuber TL, Riechmann JL, Heard JE, Jiang C, Adam LJ, Dubell AN;
PI Ratcliffe O, Pineda O, Yu G, Brown PE;
XX WPI; 2003-256576/25.
DR P-PSDB; AD837189.
XX
XX New stress-related transcription factor polynucleotides and polypeptides,
PT useful for producing transgenic plants with e.g. improved tolerance to
PT diseases or pests, decreased herbicide sensitivity, or improved nutrient
PT uptake.
XX
XX Disclosure; SEQ ID NO 127; 470pp; English.
XX
XX The invention relates to a number of cDNA sequence and their encoded
XX proteins which are especially transcription factor cDNAs and their
XX proteins. The isolated or recombinant polynucleotide is useful for
XX producing a modified plant with a modified trait, e.g. enhanced tolerance
XX to environmental conditions, improved tolerance to microbial, fungal or
XX viral diseases, improved tolerance to pest infestation, decreased
XX herbicide sensitivity, improved tolerance of heavy metals, or enhanced
XX ability to take up heavy metals, improved growth under poor
XX photoconditions, improved nutrient uptake, or reduced hormone
XX sensitivity. The transgenic plants are useful for growing a progeny plant
XX comprising the desired trait. The polynucleotides and polypeptides are
XX also useful in bioinformatic search methods. This sequence represents one
XX of the cDNAs of the invention.
XX
XX Sequence 913 BP; 249 A; 190 C; 236 G; 238 T; 0 U; 0 Other;
SQ
Query Match 16.9%; Score 134; DB 10; Length 913;
Best Local Similarity 63.8%; Pred. No. 5.4e-26;
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
QY 233 CGGAAGCTGTGAGAGATTCTGTGTGGAAACCCCGCAGAAAGCGCGCGAGAG 292
DB 271 CGGTACCTCTCCGGCGAGAAATAAATGACCTCCGGCGAGAGAGGCTCACACG 330
QY 293 GTTGTTCGAGATTGGAAACCGGTATAGAGCGCTTACGCGCGCGTGGGGAAATTG 352
DB 331 CGCGAGGAGAAAGGGGATGACAGAGAGAGAGAGAGAGCGCTGGGGAAATTG 390
QY 353 CGCGCGAGATTAAGGATCCGAAAGAAAGAGATTCAGATTGGTTGGTACATACAGA 412
DB 391 CGCGCGAGATTAGGATCCGAAAGAAAGAGATTCAGATTGGCTCGGAGATTACAGA 450
QY 413 CACCTGAGATGAGAGATTCGATTATGATGAGCGCGCTTAAATATGCGTGGAGTAAAG 472
DB 451 CGCGGAGAGACGGCGCGCTGAGTACAGAGCGCGGCTTACCTAGAGATCGAAAG 510
QY 473 CTAGGCTTAATTTCTCATATTGATTGTTGATATTTTCGAGACCGCTTAGATTAAC 532
DB 511 CTAGGCTTAATTTCTCATATTGATTGTTGATATTTTCGAGACCGCTTAGATTAAC 570
QY 533 CGAGAAAACGTTTCCCTG 550
DB 571 CTGCGCGTGGCTGCGCG 588
```

RESULT 10

```
AD141542
ID AD141542 standard; DNA; 913 BP.
XX
XX AC AD141542;
XX
XX 22-APR-2004 (first entry)
XX
XX Plant transcription factor polynucleotide #3.
XX
XX transgenic; plant; enhanced tolerance to abiotic stress;
XX glyphosphate tolerance; hormone sensitivity; disease resistance;
XX sugar sensing; flowering; flower structure; stem bifurcation;
XX branching pattern; apical dominance; trichome; stem morphology;
XX root growth; root hair; seed development; cell proliferation;
XX cell differentiation; premature senescence; necrosis; plant size;
XX leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
XX plant anthocyanin; light response; shade avoidance; bioinformatic;
XX transcription factor; gene; ds.
XX
XX Arabidopsis thaliana.
XX
XX OS
XX
XX US2004019927-A1.
XX
XX 29-JAN-2004.
XX
XX 25-FEB-2003; 2003US-00374780.
XX
XX 18-APR-2001; 2001US-00837944.
XX
XX (SHER) SHERMAN B K.
XX (RIEC) RIECHMANN J L.
XX (JIAN) JIANG C.
XX (HEAR) HEARD J E.
XX (HAAR) HAARE V.
XX (CREE) CREELMAN R A.
XX (RATC) RATCLIFFE O.
XX (ADAM) ADAM L J.
XX (REUB) REUBER T L.
XX (KEDI) KEDDIE J.
XX (BROU) BROUN P E.
XX (PILG) PILGRIM M L.
XX (DUBE) DUBELL A N.
XX (PINE) PINEDA O.
XX (YUGG) YU G.
XX
XX Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V,
XX Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE;
XX Pilgrim ML, Dubell AN, Pineda O, Yu G;
XX WPI; 2004-132245/13.
XX P-PSDB; AD141543.
XX
XX New transgenic plant comprising a recombinant polynucleotide of any one
XX of more than 500 nucleotide sequences, useful in bioinformatic search
XX methods.
XX
XX Claim 1; SEQ ID NO 5; 435BP; English.
XX
XX The invention describes a transgenic plant comprising a recombinant
XX polynucleotide of any one of more than 500 nucleotide sequences fully
XX defined in the specification or its complement. The method of the
XX invention can be used to produce a plant having altered traits such as:
XX enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone
XX sensitivity; disease resistance; sugar sensing; early or late flowering;
XX altered flower structure, change in stem bifurcations, altered branching
XX pattern, reduced apical dominance, reduced trichome density; lack of
XX trichomes; reduced ectopic trichome development; altered trichome
XX development; increase in trichome number; altered stem morphology;
XX increased root growth; increased root hairs; altered seed development;
XX altered cell proliferation or cell differentiation; rapid development;
XX premature senescence; increased necrosis; increase in seedling or plant
XX size; decreased plant size; leaf morphology; seed morphology; seed
XX biochemistry; increase in root anthocyanins; increase in plant
```

CC anthocyanins, or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This sequence encodes a plant transcription  
 CC factor that can be used in the creation of a transgenic plant with  
 CC altered traits.

XX Sequence 913 BP; 249 A; 190 C; 236 G; 238 T; 0 U; 0 Other;

Query Match 16.9%; Score 134; DB 12; Length 913;  
 Best Local Similarity 63.8%; Pred. No. 5.4e-26;  
 Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 233 CGGAAAGCTGTCAGAGATTCGTTGTGGAACCCCGCCAGAGCGCGCGAGAG 292  
 DB 271 CGGTACCTCTCCGGGAGGAAATTAAGCTCCGCGCAGAGAGAGTGGCTCAGACG 330  
 QY 293 GTTGTTCGAAGATTGGAACCGGTATTAAGCGGCTTAAGACCGCGCGCGGGAAGTTG 352  
 DB 331 CGCCGAGGAGAAAGGAGATGACAGAGAGTGGAGGAGCGCGCGGGAATTCG 390  
 QY 353 CGGCGAGATTAAGGATCCGAAAAAGAAAGATTCGATTTGGTGTACATACGAGA 412  
 DB 391 CGCGGAGATTAAGGATCCGAAAAAGAAAGATTCGATTTGGTGTACATACGAGA 450  
 QY 413 CACCTGAGATGAGCATTCGTTATGATGACCGCGCTTAATATGCGTGAAGCTAAG 472  
 DB 451 CGCCGAGGAGCGCGGCGGTGGCGTACGACGAGCGCGCTTACGATCAGAGATGAAAG 510  
 QY 473 CTAGGCTTAATTTCTCTCATTTGATTGTTCCGAATTTTCCGAGCCGTTAAGTAAAC 532  
 DB 511 CTAAAGCTGAATTTCCGCAATTGATTGTTCTTGAATGATAGCCGTTAAGATTAGGC 570  
 QY 533 CGAGAAACGTTCCCTG 550  
 DB 571 CTGCGCGTGGCTGCGCG 588

# RESULT 11

AD001614  
 ID AD001614 standard; cDNA; 913 BP.

XX AD001614;

DT 01-JUL-2004 (first entry)

XX Thalecress transcription factor cDNA #14.

KW Thalecress; transcription factor; ss; gene; plant; transgenic;  
 KW abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;  
 KW phosphate limitation; potassium limitation; nitrogen limitation;  
 KW hormone sensitivity; disease resistance; sugar sensing; seed germination;  
 KW flowering; inflorescence architectural change;  
 KW meristem cell differentiation; phyllotaxy; apical dominance;  
 KW trichome development; seed development; premature senescence;  
 KW delayed senescence; lethality; necrosis; plant size; leaf morphology;  
 KW seed morphology; secondary metabolism; light response; shade avoidance.

XX Arabidopsis thaliana.

OS US2004045049-A1.

PN 04-MAR-2004.

PD 10-APR-2003; 2003US-00412699.

XX 13-SEP-1999; 90US-00394519.

PR 21-JAN-2000; 2000US-00489376.

PR 17-FEB-2000; 2000US-00506720.

PR 22-MAR-2000; 2000US-00533591.

PR 22-MAR-2000; 2000US-00533029.

PR 22-MAR-2000; 2000US-00533030.

PR 22-MAR-2000; 2000US-00533392.

PR 06-APR-2000; 2000WO-US009448.  
 PR 16-NOV-2000; 2000US-00713994.  
 PR 27-MAR-2001; 2001US-00819142.  
 PR 17-APR-2001; 2001US-00837444.  
 PR 30-JUN-2002; 2002US-00958131.  
 PR 14-JUN-2002; 2002US-00171468.  
 PR 09-AUG-2002; 2002US-00225066.  
 PR 09-AUG-2002; 2002US-00225067.  
 PR 09-AUG-2002; 2002US-00225068.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 25-FEB-2003; 2003US-00374780.

XX (ZHAN/) ZHANG J.  
 PA (FROM/) FROMM M E.  
 PA (HEAR/) HEARD J E.  
 PA (RIE/) RIECHMANN J L.  
 PA (ADAM/) ADAM L J.  
 PA (BROU/) BROUN P E.  
 PA (PINE/) PINEBA O.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J S.  
 PA (YUG/) YU G.  
 PA (JIANG/) JIANG C.  
 PA (SAMA/) SAMAHA R S.  
 PA (PILG/) PILGRIM M L.  
 PA (CREE/) CREELMAN R A.  
 PA (DUBB/) DUBELL A N.  
 PA (BATC/) BATCLIFFE O.  
 PA (KUMI/) KUMIMOTO R.  
 PA (SHER/) SHERMAN B K.

XX Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Brown PE;  
 PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS;  
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;  
 PI Sherman BK;

XX WPI; 2004-225755/21.  
 DR P-PSDB; AD001615.

PT New transgenic plant, useful in developing phenotypes with altered or  
 PT improved characteristics or traits.

XX Claim 1, SEQ ID NO 27; 213pp; English.

XX The invention relates to a transgenic plant comprising a recombinant  
 CC polynucleotide having a polynucleotide sequence or its complementary  
 CC sequence comprising a sequence encoding a polypeptide, that initiates  
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,  
 CC Rice, Rape or Corn, comprising any of the sequences appearing as AD001588  
 CC -AD003527 or AD003530-AD003559. Also included are using a transgenic  
 CC plant to grow a progeny plant, an expression cassette (comprising a  
 CC constitutive, inducible or tissue-specific promoter and a recombinant  
 CC polynucleotide described above), a host cell comprising the expression  
 CC cassette, producing a modified plant having a modified trait, identifying  
 CC a factor that is modulated by or interacts with a polypeptide encoded by  
 CC the polynucleotide sequence and identifying at least one downstream  
 CC polynucleotide sequence that is subject to a regulatory effect of any of  
 CC the polypeptides encoded by the polynucleotide described above. The  
 CC transgenic plant is useful for producing a plant that has an altered  
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance  
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance  
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to  
 CC salt, tolerance to phosphate limitation, tolerance to potassium  
 CC limitation, decreased sensitivity to nitrogen limitation), altered  
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered  
 CC response to ethylene, disease resistance, altered susceptibility to  
 CC Brevia, altered susceptibility to Fusarium, altered susceptibility to  
 CC susceptibility to Sclerotinia, altered sugar sensing, improved seed  
 CC germination and seedling vigor, early flowering, late flowering, extended  
 CC period of flowering, an inflorescence architectural change, a change in  
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell  
 CC differentiation, altered phyllotaxy, altered branching pattern, reduced

CC apical dominance, reduced trichome density, ectopic trichome development,  
 CC altered trichome development, altered stem morphology, increased root  
 CC growth, increased root hairs, altered stem morphology, altered cell  
 CC proliferation/cell differentiation, premature senescence, delayed  
 CC senescence, lethality, increased necrosis, an increase in seedling or  
 CC plant size, decreased plant size, a change in leaf morphology, increased  
 CC altered leaf development, increased leaf size and mass, glossy leaves,  
 CC leaf cell expansion, change in seed morphology, altered seed coloration,  
 CC increased seed size, decreased seed size, altered seed shape, change in  
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid  
 CC content, increased leaf insoluble sugars, decreased leaf insoluble  
 CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid  
 CC content, an alteration of leaf glucosinolate content, change in seed  
 CC biochemistry, an increase in seed oil content, decrease in seed oil  
 CC content, increase in seed fatty acid content, decrease in seed fatty acid  
 CC content, increase in seed protein content, decrease in seed protein  
 CC content, alteration in seed prenyl lipid content, increase in seed  
 CC sterols, upregulation of genes involved in secondary metabolism, increase  
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in  
 CC light response or shade avoidance. The present sequence encodes a  
 CC thalictress transcription factor of the invention.

Sequence 913 BP; 249 A; 190 C; 236 G; 238 T; 0 U; 0 Other;

Query Match 16.9%; Score 134; DB 12; Length 913;  
 Best Local Similarity 63.8%; Pred. No. 5.4e-26;  
 Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 233 CGGAAAGCTGTGAGAGATTCTGTGTGGAAACCCGCGAGAGCGCGCGAGAG 292  
 DB 271 CGTTACTCTCCGCGAGAGAAATATAGCTCCGCGAGAGAGAGGTGCTCACAG 330  
 QY 293 GTTGTTCGAGAGATTGGAACCGGTATAGAGCGGTAGACCGCGCGGTGGGAGTTGC 352  
 DB 331 CGCGAGGAGGAGGAGATGCAAGTACAGAGAGTGAAGAGAGCGCGGTGGGAGAAATTCG 390  
 QY 353 CGCGAGAGATTAAGAGATTCGAAAGAAAGATCCAGATTTGGTGGTATACGAGA 412  
 DB 391 CGCGAGAGATTAGGATTCGAAAGAAAGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 450  
 QY 413 CACCTGAGAGATGAGATTTGGTATGATGACCGCGGTAAATATGCGTGAAGCTAAG 472  
 DB 451 CGCGAGAGAGCGCGGTGGGCTGACGACCGAGCGGCTTCAAGTCAAGAGATTCGAAAG 510  
 QY 473 CTAGGTTAATTTCTCATTTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 532  
 DB 511 CTAGGTTAATTTCTCATTTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 570  
 QY 533 CGAGAAACGTTTCCTG 550  
 DB 571 CTGCGCGTGGTGGCGG 588

## RESULT 12

AAA53744  
 ID AAA53744 standard; DNA; 885 BP.

AAA53744;

19-DEC-2000 (first entry)

Plant transcription factor AP2 domain.

AP2; transcription factor; plant metabolism; metabolite; primary;  
 secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;  
 food colouring; flavouring; fragrance; antimicrobial; pathogenic;  
 insecticide; gene expression; modulation; ds.

Catharanthus roseus.

Key Location/Qualifiers  
 CDS 9..641  
 FT /\*tag= a

/product= "AP2 polypeptide"

FT W0200046383-A2.  
 XX 10-AUG-2000.  
 PD 07-FEB-2000; 2000MO-NL000075.  
 XX 05-FEB-1999; 99DK-00000158.  
 PR 10-FEB-1999; 99US-0119388P.  
 XX (VLE-) RIJMSUNIV LEIDEN.  
 PI Memelink J, Van Der Fits CTR, Menke FLH, Kijne JW;  
 XX WPI, 2000-499380/44.  
 DR P-P-SDB; AA97227.  
 XX  
 PT Modulating level of metabolites and stress resistance in recombinant  
 PT cells for synthesis of plant metabolites such as alkaloids including  
 PT terpenoid indole alkaloids, by providing transcription factor to the  
 PT cell.

Disclosure; Page 95; 101pp; English.

CC Many plant secondary metabolites have value as pharmaceuticals, food  
 CC colourings, flavours and fragrances. Some plant secondary metabolites are  
 CC linked to plant or plant cell defence mechanisms and may confer to the  
 CC plant antimicrobial activity, protection against UV light, herbivores,  
 CC pathogens, insects and nematodes. Plant secondary metabolites such as  
 CC terpenoid indole alkaloids (TIA) represent a class of pharmaceutically  
 CC useful compounds which naturally occur in many plant species. New methods  
 CC are described which modulate the expression of one or more genes involved  
 CC in the biosynthesis of plant metabolites or their precursors in plant  
 CC cells. The method comprises inserting into a plant cell a sequence  
 CC encoding a transcription factor comprising an AP2 DNA-binding domain and  
 CC by modifying the expression of that transcription factor. Transcription  
 CC factors comprising an AP2 DNA-binding domain are useful as central  
 CC regulators of complex metabolite pathways involving numerous target genes  
 CC for such transcription factors. This means that the yield of commercially  
 CC valuable metabolite compounds can be enhanced and the tolerance of plants  
 CC towards exogenous stress factors can be influenced. The method is useful  
 CC for modulating the level of one or more metabolites. By providing a  
 CC transcription factor to the cell the level of the metabolite is enhanced  
 CC by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to  
 CC a cell to which the transcription factor is not provided

Sequence 885 BP; 279 A; 151 C; 175 G; 280 T; 0 U; 0 Other;

Query Match 16.7%; Score 132.6; DB 3; Length 885;  
 Best Local Similarity 74.5%; Pred. No. 1.3e-25;  
 Matches 181; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 302 AGGATGGAACCGGTATTAAGGCGGTAGACGGCGCGCGGAGGAAAGTTCCGCGCGGAGA 361  
 DB 373 AGGATGGAATTAGTACCGTGGCGGTAGACGGCGCGCATGAGGAAATTCGCTGCCGAA 432  
 QY 362 TAAGGATCGAAGAAAGAAAGATCCAGATTTGTTGGTATCATACGAGACCTTAGG 421  
 DB 433 TCAGGGATCCCAAGAGAAAGATGAGATTTGTTGGTAACTTACGAGACGGCGGAG 492  
 QY 422 ATGACGATTTGGTATGATGACCGCGGTAAATATGCTGAGAGCTAAGAGCTTA 481  
 DB 493 ATGCGGATTTAGTATGATGACCGCGGTAAATATGCTGAGAGCTAAGAGCTTA 552  
 QY 482 ATTTTCCTATTGATTTGTTGGAATATTTCCGAGCCGTTAGAGTAACCGAGAAAC 541  
 DB 553 ATTTCCCAATCTATTGTTGTTGCTAAAT---CTCCGTTAGAGTAAGTCTTAAGCGCC 609  
 QY 542 GTT 544  
 DB 610 GAT 612

RESULT 13  
ID AAZ50843 standard; DNA; 708 BP.  
XX  
AC AAZ50843;  
XX  
DT 31-MAY-2000 (first entry)  
XX  
DE Tobacco salicylic acid inducible gene C18-1.  
XX  
KW Tobacco plant; salicylic acid inducible gene; fungal pathogen;  
KM SA-inducible gene; transgenic plant; pathogen resistance; C18-1 gene; ds.  
XX  
OS Nicotiana tabacum.  
XX  
PN WO200008186-A1.  
XX  
PD 17-FEB-2000.  
XX  
PF 02-AUG-1999; 99WO-EP005581.  
XX  
PR 03-AUG-1998; 98US-0095187P.  
XX  
PA (MOGE-) MOGEN INT NV.  
XX  
PI Stuiver MH, Jepson I, Horvath DM, Chua N;  
XX  
DR WPI; 2000-205725/18.  
XX  
PT Novel salicylic acid inducible genes from tobacco plants, useful for  
PT making transgenic plants with enhanced pathogenic resistance.  
XX  
PS Claim 1, Page 44; 57pp; English.  
XX  
CC The patent discloses fifteen new salicylic acid (SA) inducible genes from  
CC Nicotiana tabacum, which were identified by differential display PCR.  
CC Nine of these genes were subcloned and sequenced. Based on different  
CC kinetics of induction response, these genes were classified into four  
CC categories, class I, II, III and IV response genes. The SA-inducible  
CC genes are useful for making transgenic plants with enhanced pathogen  
CC resistance. The plants incorporating these genes show reduced  
CC susceptibility to fungal pathogens. The present sequence is a  
CC specifically claimed SA-inducible gene C18-1 from N. tabacum, which  
CC belongs to class I  
XX  
SQ Sequence 708 BP; 205 A; 124 C; 196 G; 183 T; 0 U; 0 Other;  
XX  
Query Match 16.3%; Score 129.4; DB 3; Length 708;  
Best Local Similarity 64.2%; Pred. No. 8.6e-25;  
Matches 210; Conservative 0; Mismatches 116; Indels 1; Gaps 1;

245 AGGAGGATTCGTGTGGGAAACCCCGCAGAGCGGCGCGGAGAGGTTGTCGAAG 304  
145 AGAGGAAATTTGTTGTTCCACGATACAAAGCGCGCGCGGCTGAATTACGA 204  
305 ATTGGAACCGGTATTAAGGCGCTTGAACGGCGCTTGGGGAAGTTCCCGCGAGTTAA 364  
205 GGGGAAAGGCAATTACAGAGGTGTGACGACGCGCTTGGGGAATTGCGCGGAGTTTA 264  
365 GGGATCCGAAAGAAAGAGATCCA-GGATTTGTTGGGTATCATTCGAGACCTGAGAGAT 423  
265 GGGATCCGCGGAGAAATGAGACTTGGGTTTGGCTTGAACATACGAAACGATGAGAT 324  
424 GCAGCATTTGGCTTATGATGACGCGCTTATATATGCGTGAAGCTAAAGCTTAAT 483  
325 GCGCATTTGCTTATGATTAAGCGCTTATATGATGCGTGAAGGCTCATTTAAT 384  
484 TTTCCTCATTTGATTTGTTGCAATATTTCCGAGCCCGTTAGATTAACCGAGAAACGT 543  
385 TTTCACATAGAGATCGGTTTAAATGAACCGGAAACCGGTTCAATTACGCGGAAAGCGA 444  
544 TTCCCTCGGAGCCTTACGACGCTCG 570

Db 445 GCGTCGCTGAACCGGCTAGTTCCGTCG 471  
RESULT 14  
ADJ10797  
ID ADJ10797 standard; DNA; 437 BP.  
XX  
AC ADJ10797;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Recombinant tomato DNA to generate disease resistant plants SeqID 193.  
XX  
KW genetically engineered; plant; Avr-Pto; avirulent Pto;  
KM bacterial speck disease; tomato; transgenic; biotic; abiotic stress; ds;  
XX  
PW Pfl.  
XX  
OS Lycopersicon esculentum.  
XX  
PN US2004006787-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 14-JAN-2003; 2003US-00341961.  
XX  
PR 14-JAN-2002; 2002US-0348792P.  
XX  
PA (MART/) MARTIN G B.  
PA (MYSO/) MYSORE K K.  
PA (CRAS/) CRASTA O R.  
PA (FOLK/) FOLKERTS O.  
PA (SWIR/) SWIRSKY P.  
XX  
PI Martin GB, Mysore KK, Crasta OR, Folkerts O, Swirsky P;  
XX  
DR WPI; 2004-081759/08.  
XX  
PT New genetically engineered plant comprising a recombinant polynucleotide  
PT showing expression associated with Avr-Pto mediated defense response,  
PT useful in increasing resistance of plant against bacterial speck disease.  
XX  
PS Claim 5; SEQ ID NO 193; 176pp; English.  
XX  
CC This invention relates to a method of generating novel genetically  
CC engineered plants. Specifically, it refers to compositions useful for  
CC transforming plants with a recombinant polynucleotide or plant gene that  
CC shows a specific pattern of expression associated with the Avr-Pto  
CC mediated defense response. Avr-Pto is described as the avirulent Pto gene  
CC found in Pseudomonas syringae pathovar tomato strain T1(A1),  
CC which mediates bacterial speck disease in tomato plants. The present  
CC invention describes identifying genes that are up- or down-regulated in  
CC the defense response and that are involved in the interaction of Avr-Pto  
CC with Pto and/or Pfl. As such, these novel recombinant polynucleotides  
CC can be used to generate transgenic plants that are resistant to bacterial  
CC speck disease and furthermore exhibit increased resistance against biotic  
CC and abiotic stresses. This polynucleotide sequence is a recombinant  
CC tomato polynucleotide used to generate genetically engineered, disease  
CC resistant plants of the invention.  
XX  
SQ Sequence 437 BP; 140 A; 79 C; 123 G; 95 T; 0 U; 0 Other;  
XX  
Query Match 16.2%; Score 128.6; DB 12; Length 437;  
Best Local Similarity 69.0%; Pred. No. 1.2e-24;  
Matches 176; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

316 TATTAAGGCGTTAGAGCGGCGCGTGGGGAAGTTGCGCGGAGATTAAGGATCCGAAA 375  
10 TATAGAGGCGTTAGAGCGGCGCGTGGGGAAGTTGCGCGGAGATTAAGGATCCGAGG 69  
376 AAGAAAGATCCAGATTTGTTGGGTACATACGACACCTGAGGATCCAGCATTTGCT 435

Db 70 AAGACGAGCTTAGGTTGGCTTGGAACGTACGAAAACAGCTGAAGAGCTGCATTGCT 129  
 QY 436 TATGATGACGCGCGCTTTAATATGCGTAGAGCTAAAGCTAGCTTAATTTTCTCATTTG 495  
 Db 130 TATGATTAAGAGCTCTTATGAAATGAGAGATCAAAAGACATTGATTTCCGCGACCGG 189  
 QY 496 ATTGTTGCAATATATTTCCGACCCCGTTAGAGTAACCCGAGAAAAGCTTTCCCTGGCGAG 555  
 Db 190 ATCGGTTTGAATGAACCGGACCGGTTTCAGATTACCGCGGAAAAGCGAGATGCGCGGAA 249  
 QY 556 CCTTTCAGACGTCG 570  
 Db 250 CCGGCAAGCTCGTCG 264

RESULT 15  
 ID ADKS9746  
 ADKS9746 standard; DNA; 694 BP.  
 AC ADKS9746;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Plant DNA sequence which confers altered metabolic characteristic #7129.  
 XX  
 KW altered metabolic characteristic; plant; acid metabolism;  
 KW alcohol metabolism; fatty acid metabolism;  
 KW branched fatty acid metabolism; alkaloid metabolism;  
 KW amino acid metabolism; ester metabolism; glyceride metabolism;  
 KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;  
 KW terpene metabolism; isoprenoid metabolism; alkene metabolism;  
 KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
 KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.  
 XX  
 OS Unidentified.  
 OS  
 PN WO2003020936-A1.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 30-AUG-2002; 2002WO-US027884.  
 XX  
 PR 31-AUG-2001; 2001US-0316471P.  
 XX  
 PA (DOMC ) DOW CHEM CO.  
 PA (DOMC ) DOW AGROSCIENCES LLC.  
 XX  
 PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;  
 PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Muller BA;  
 DR WPT, 2003-313091/30.  
 XX  
 PT Novel genes that confer altered metabolic characteristics in Nicotiana  
 PT benthamiana plants, useful for altering the levels of metabolites e.g.  
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.  
 XX  
 PS Claim 1; SEQ ID NO 7129, 2576bp; English.  
 XX  
 CC The invention comprises DNA sequences which confer an altered metabolic  
 CC characteristic when they are expressed in a plant. The DNA sequences of  
 CC the invention are useful for producing plants with an altered metabolic  
 CC characteristic, such as: altered acid metabolism, alcohol metabolism,  
 CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other  
 CC base metabolism, altered amino acid metabolism, altered ester metabolism,  
 CC altered glyceride metabolism, altered phenolic metabolism, altered  
 CC carbohydrate metabolism, altered sterol, oxygenated terpene, or  
 CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon  
 CC metabolism, ketone or quinone metabolism. The DNA sequences of the  
 CC invention may be used to provide disease resistance in a plant and gene  
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a  
 CC DNA sequence of the invention.  
 XX  
 SQ Sequence 694 BP; 220 A; 137 C; 184 G; 153 T; 0 U; 0 Other;

Query Match 16.1%; Score 127.6; DB 10; Length 694;  
 Best Local Similarity 57.9%; Pred. No. 2.7e-24;  
 Matches 226; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 228 AATGCGGAAAGCTGTCAAGAGATTCGTGTGGAAACCCGCGAAGCGCGCGC 287  
 Db 275 AAATCGAGCCAAAGGAGAGGAATTTGTGTCCCGCGGAGACAAACGCGCGC 334  
 QY 288 AGAGGTTGTTCAAGGATTGGAACCGGTATAAGGCGCTTAGACGCGCGCGTGGAGAA 347  
 Db 335 GCGCACTGAGATACCGAGGGGAAAGCATTAAGAGGTTAGACGACGCGCGTGGAGAA 394  
 QY 348 GTTCGCGCGGAGATTAAGGATCCGAAAAGAAAGATCCAGATTGTGTGCTACATA 407  
 Db 395 ATTTGCGGCGAGATTAGAGATCCGCGAAGAAATGAGCTAGGGTTTGCTTGGAAACATA 454  
 QY 408 CGAGACACCTGAGATGACAGATTTGCTTATGATGAGCGCGCTTAATATGCGTGAGC 467  
 Db 455 CGAAACAGATGAAGAGCTGCAATTGCTTATGATTAAGCGGCTTATGAAATGCGGTTTC 514  
 QY 468 TAAAGCTAGGCTTAATTTTCTCATTTGATTGTGTAATTTCCGACCCGTTAGAGT 527  
 Db 515 AAAGCTCATTTAAATTTTCCACATGAAATCGGTTAAATGAACCGAACCAGTTGAGT 574  
 QY 528 AAACCGAAGAAAGCTTTCCCTGCGAGCCTTCTAGAGCTGCTCTTCTTCTTC 587  
 Db 575 CACGGGAAAGAGCGAGCATTCGCTGAAACCGGCTAGTTGTGGAAAATAGTTCACTTA 634  
 QY 588 TTGCTGAAATAATGAGAGAAAGAA 617  
 Db 635 ACGGAGAAAGAAAGCTGTTGACGTGAGAA 664

Search completed: March 7, 2005, 17:11:36  
 Job time : 565 secs

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US-09-533-029-33
; Sequence 33, Application US/09533029
; Patent No. 6664446
;
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Brown, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MI-010
;
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 33
; LENGTH: 913
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1006
;
US-09-533-029-33

```

Query Match	14.0%;	Score 110.6;	DB 4;	Length 913;
Best Local Similarity	62.5%;	Pred. No. 1.3e-22;		
Matches 173; Conservative	0;	Mismatches 104;	Indels 0;	Gaps 0;

Qy	309	GAACCGGTTATPAAGGGCGTTAGACGGCGGGCGTGGGGGAAAGTTCCGGCGGAGATPAAGGA	368
Db	393	GAAGCATTTACAGAGAGTAGAGGACCGATGGGGGAAATTCGGCGCGAGATACGTGA	452
Qy	369	TCCGAAAAAAGATTCAGAGATTTGGTTGGGTACATACGAGACCTGAGATGCAGC	428
Db	453	TCCGGCGCAAAATGAGAGCTAAGGGTTTGGTTAAGGACGTTGAGACGGCGGAAGATCGCGC	512
Qy	429	ATTGGCTTATGATGCAGCCGCTTTAATATGGGTGAGAGCTAAGCTAGCTTAATTTCC	488
Db	513	TTTAGCTTACGATATAGCTGCTTTAGAGATGGGTGGTTCGCGGCTTTATGAATTTCC	572
Qy	489	TCATTTGATTTGGTTCGATATTTCCGGACCCGTTAGATGAACCCGAGAAAACGTTTCC	548
Db	573	GTTGAGGGTTAATTCGGGTGAACCTGACCCGGTGGGATCAAGCTTAAGATCTTCTTC	632
Qy	549	TGGGAGCCTTCTTACGACGTCGTCGCTCTTCTTCTT	585
Db	633	GTCGTGTCGTGTCGTCTCTTCTTCAAGTCGTCGCTT	669

RESULT 3  
US-09-533-023-17  
Sequence 17, Application US/095330229  
Patent No. 6664446  
GENERAL INFORMATION:  
APPLICANT: Heard, Jacqueline  
APPLICANT: Brown, Pierre  
APPLICANT: Reichmann, Josee-Luis  
APPLICANT: Keddie, James  
APPLICANT: Pineda, Omaira  
APPLICANT: Adam, Luc  
APPLICANT: Samaha, Raymond  
APPLICANT: Zhang, James  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ratcliffe, Oliver

? APPLICANT: Pilgrim, Marsha  
 ? APPLICANT: Jiang, Cai-zhong  
 ? TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDE  
 ? FILE REFERENCE: MRI-010  
 ? CURRENT APPLICATION NUMBER: US/09/533,029  
 ? CURRENT FILING DATE: 2000-03-22  
 ? EARLIER APPLICATION NUMBER: 60/125,814  
 ? EARLIER FILING DATE: 1999-03-23  
 ? NUMBER OF SEQ ID NOS: 121  
 ? SOFTWARE: PatentIn Ver. 2.1  
 ? SEQ ID NO 17  
 ? LENGTH: 964  
 ? TYPE: DNA  
 ? ORGANISM: *Arabidopsis thaliana*  
 ? FEATURE:  
 ? OTHER INFORMATION: G28  
 ? US-09-533-029-17

Query Match	13.1%;	Score 103.6;	DB 4;	Length 964;
Best Local Similarity	63.8%;	Pred. No. 1.6e-20;		
Matches 157; Conservative	0;	Mismatches 89;	Indels 0;	Gaps 0;

Oy	CGAAGATTGGAA	CCGGTATAAGGGCGTTAG	CCGGCGCGCGCGTGGAGGAAGTTCCGGCGG	358	
Oy	299				
Db	CGCGAAGGAAGA	GCATTATAGAGAGTGA	CAAAAGCCCTGGGGGAATTTGGCGCGG	546	
Db	487				
Oy	359	AGATTAAGGATCCGAAAA	AAAAAGATCAAGATTGGTTGGGTACATACGAGCACCTG	418	
Oy					
Db	547	AGATTGAGAATCCGGCGA	GAAGACGATAGGGTTTGGTTAGAACGTTTGAAGACCGCGG	606	
Oy	419	AGATACAGATTTGGCTTAT	TGATGAGCGCGGTTTAATATCCGAGAGCTAAAGCTAGGC	478	
Db	607	AGAGCGCGCGCTTGCTTAC	GAACAAGCTGCTTTCAGGATGCGTGGTTCCCGCGCTTTGT	666	
Oy	479	TTAATTTTCCTATTGATT	GGTTGCAATATTTTCGGA	CCCGTTAGAGTAAACCCGAGAA	538
Db	667	TGAATTTTCGGTTAGAG	ATTATATCAGAGAAACCGGACCGCGTTGCAATCAAGTCMAAGA	726	
Oy	539	AACGTT	544		
Db	727	GATCTT	732		

```

RESULT 4
US-09-202-161B-19
; Sequence 19, Application US/09202161B
; Patent No. 6653533
; GENERAL INFORMATION:
; APPLICANT: Purdue Research Foundation
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: 7024-371
; CURRENT APPLICATION NUMBER: US/09/202,161B
; CURRENT FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: PCT/US97/10382
; PRIOR FILING DATE: 1997-06-12
; PRIOR APPLICATION NUMBER: 60/046,494
; PRIOR FILING DATE: 1997-05-14
; PRIOR APPLICATION NUMBER: 60/019,633
; PRIOR FILING DATE: 1996-06-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: ASCII
; SEQ ID NO 19
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-202-161B-19

```

Query Match	13.0%	Score 102.6	DB 4	Length 177
Best Local Similarity	74.6%	Pred. 1.3e-20		
Matches 129	0	Mismatches 44	Indels 0	Gaps 0
316	TATTAAGGGGCTTACAGCGGCGCCCTGGGGGAAATTGCGGCGGAGATTAAGGATCCGAAA			375



```
Db      4 TATAGAGCGCTTACAGACGCTCCGTGGGGGAAATTTGGCGGAGATTAAGATTCGGCG 63
QY      376 AAGAAAGATCCAGATTTGGTGGTACATACGACACCTAGAGATGACGATTGGCT 435
Db      64 AAGACGGAGCTTGAGGCTTGGCTTGGACGTAACGAAACAGCTAAGAGAGCTGCAATTGGCT 123
QY      436 TATGATGACGCGCGCTTATATATGCGTGAAGCTTAAGCTTAAGCTTAATTTTCC 488
Db      124 TATGATTAAGCTCTTATATGATGAGAGATCAAAAGACATTGAAATTTCCC 176

RESULT 5
US-09-202-161B-20
; Sequence 20, Application US/09202161B
; Patent No. 6653533
; GENERAL INFORMATION:
; APPLICANT: Purdue Research Foundation
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: 7024-371
; CURRENT APPLICATION NUMBER: US/09/202,161B
; CURRENT FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: PCT/US97/10382
; PRIOR FILING DATE: 1997-06-12
; PRIOR APPLICATION NUMBER: 60/046,494
; PRIOR FILING DATE: 1997-05-14
; PRIOR APPLICATION NUMBER: 60/019,633
; PRIOR FILING DATE: 1996-06-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: ASCII
; SEQ ID NO 20
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-202-161B-20

Query Match      10.9%; Score 86.6; DB 4; Length 177;
Best Local Similarity 68.8%; Pred. No. 7.5e-16;
Matches 119; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY      316 TATAGAGCGCTTACAGACGCTCCGTGGGGGAAATTTGGCGGAGATTAAGATTCGAA 375
Db      4 TACAGAGAGATACAGAGCTGCTCGTGGGGAAATAGCTCGGAAATTCGCAATTCGGCT 63
QY      376 AAGAAAGATCCAGATTTGGTGGTACATACGACACCTAGAGATGACGATTGGCT 435
Db      64 AAGACGGAGCTTGAGGCTTGGCTTGGACGTAACGAAACAGCTAAGAGAGCTGCAATTGGCT 123
QY      436 TATGATGACGCGCGCTTATATATGCGTGAAGCTTAAGCTTAAGCTTAATTTTCC 488
Db      124 TATGATTAAGCTCTTATATGATGAGAGATCAAAAGACATTGAAATTTCCC 176

RESULT 6
US-09-202-161B-5
; Sequence 5, Application US/09202161B
; Patent No. 6653533
; GENERAL INFORMATION:
; APPLICANT: Purdue Research Foundation
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: 7024-371
; CURRENT APPLICATION NUMBER: US/09/202,161B
; CURRENT FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: PCT/US97/10382
; PRIOR FILING DATE: 1997-06-12
; PRIOR APPLICATION NUMBER: 60/046,494
; PRIOR FILING DATE: 1997-05-14
; PRIOR APPLICATION NUMBER: 60/019,633
; PRIOR FILING DATE: 1996-06-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: ASCII
; SEQ ID NO 5
; LENGTH: 761
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```
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-202-161B-5

Query Match      10.9%; Score 86.6; DB 4; Length 761;
Best Local Similarity 68.8%; Pred. No. 1.7e-15;
Matches 119; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY      316 TATAGAGCGCTTACAGACGCTCCGTGGGGGAAATTTGGCGGAGATTAAGATTCGAA 375
Db      176 TACAGAGAGATACAGAGCTGCTCGTGGGGAAATAGCTCGGAAATTCGCAATTCGGCT 235
QY      376 AAGAAAGATCCAGATTTGGTGGTACATACGACACCTAGAGATGACGATTGGCT 435
Db      236 AAGACGGAGCTTGAGGCTTGGCTTGGACGTAACGAAACAGCTAAGAGAGCTGCAATTGGCT 295
QY      436 TATGATGACGCGCGCTTATATATGCGTGAAGCTTAAGCTTAAGCTTAATTTTCC 488
Db      296 TATGATTAAGCTCTTATATGATGAGAGATCAAAAGACATTGAAATTTCCC 348

RESULT 7
US-09-640-211A-1401/C
; Sequence 1401, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1401
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1401

Query Match      10.2%; Score 80.4; DB 4; Length 481;
Best Local Similarity 67.1%; Pred. No. 9.1e-14;
Matches 114; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY      321 GGGCGTTAGACGCGCGCGCGGGAAGTTCCGGCGGAGATTAAGGATCCGAAAGAA 380
Db      480 GGGCGTGCCTCGCGCGCGCGGGAAGTTCCGGCGGAGATTAAGGATCCGAAAGGCA 421
QY      381 AGGATCAGAGATTGGTGGTACATACGACACCTGAGATGACGATTGGCTTATGA 440
Db      420 GGGGACGCGCGTGTGCTGGGACGTTGACACGCGGAGGAGGAGCGGAGGCTTACGA 361
QY      441 TGCAGCGCGTTTATATATGCGTGAAGCTTAAGCTTAAGCTTAATTTTCTC 490
Db      360 CCGCGCGCGTTTCAAGCTCCGCGGAGCAAGGCAATCTGAATTCCTCCG 311

RESULT 8
US-09-533-029-11
; Sequence 11, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Brown, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
```



Query Match 9.2%; Score 72.6; DB 4; Length 390;  
Best Local Similarity 56.8%; Pred. No. 1.7e-11;  
Matches 154; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

QY 238 AGCTTCAGAGAGATTCTGTTGGGAAACCCCGCAGAGAGCGCGCGAGAGAGTTGT 297  
DB 48 AGAAGTGAAGGTGATTCCTCTTGGAGATGTGAGAGGATCCACACCAGATTGGGGGG 107  
QY 298 TCAGAGATTGGAACCGGTAAAGGGCGGTAGACGGGGCGCGCGGGGAAAGTTGGCGCG 357  
DB 108 AGAAGAGAAAAATGTTTACAGAGGTATCAGACAGGCTTCATGCGGAAAAATGGGCTGCG 167  
QY 358 GAGATTAAGGATCCGAAAAAGATCCAGATTGTTGGGTATACATACAGACACT 417  
DB 168 GAGATTGAGATCCAGTAAG---GGGGTAAAGGTTTGGCTTGAAGCTTCAACAGCGCA 224  
QY 418 GAGATGACAGATTGGCTTATGATGACGGCGGCTTAAATATGCTGAGCTAAAGCTAAG 477  
DB 225 GAGAGAGCCCGCAAGGCTATGATGACGGCGCTAAAGATCCAGAGTAAGAAAGCTAAG 284  
QY 478 CTTAATTTCTCATTTGATTGTTGTAATA 508  
DB 285 CTTAATTTGCTGATTAATCTGTTCTGTTA 315

## RESULT 12

US-09-640-211A-549  
; Sequence 549, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE REFERENCE: 11000.1021CIU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; LENGTH: 1163  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-09-640-211A-549

Query Match 9.2%; Score 72.6; DB 4; Length 1163;  
Best Local Similarity 56.8%; Pred. No. 3.1e-11;  
Matches 154; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

QY 238 AGCTTCAGAGAGATTCTGTTGGGAAACCCCGCAGAGAGCGCGCGAGAGAGTTGT 297  
DB 373 AGAAGTGAAGGTGATTCCTCTTGGAGATGTGAGAGGATCCACACGATTGGGGGG 432  
QY 298 TCAGAGATTGGAACCGGTAAAGGGCGGTAGACGGGGCGCGGGGAAAGTTGGCGCG 357  
DB 433 AGAAGAGAAAAATGTTTACAGAGGTATCAGACAGGCTTCATGCGGAAAAATGGGCTGCG 492  
QY 358 GAGATTAAGGATCCGAAAAAGATCCAGATTGTTGGGTATACATACAGACACT 417  
DB 493 GAGATTGAGATCCAGTAAG---GGGGTAAAGGTTTGGCTTGAAGCTTCAACAGCGCA 549  
QY 418 GAGATGACAGATTGGCTTATGATGACGGCGGCTTAAATATGCTGAGCTAAAGCTAAG 477  
DB 550 GAGAGAGCCCGCAAGGCTATGATGACGGCGCTAAAGATCCAGAGTAAGAAAGCTAAG 609  
QY 478 CTTAATTTCTCATTTGATTGTTGTAATA 508  
DB 610 CTTAATTTGCTGATTAATCTGTTCTGTTA 640

## RESULT 13

US-09-640-211A-570  
; Sequence 570, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE REFERENCE: 11000.1021CIU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; LENGTH: 447  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-09-640-211A-570

Query Match 9.1%; Score 72.2; DB 4; Length 447;  
Best Local Similarity 62.9%; Pred. No. 2.4e-11;  
Matches 129; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 292 GGTGTTCCGAGATTGGAACCGGTAAAGGGGCTTAGACGGGGCGCGGGGAAAGTTC 351  
DB 65 GGTATTGCAAGGCTCCGCAAGCTCTACAGAGGTGAGACAGAGGCACTGGGGGAAATGG 124  
QY 352 GCGCGGAGATTAAGGATCCGAAAAAGATCCAGATTGTTGGGTATACATACAG 411  
DB 125 GTAGCAGAGATCAGATTACC---TAGGAATAGAACCAAGCTCTGGCTTGAACCTTTGAC 181  
QY 412 ACACTGAGATCAGAGATTGCTTATGATGACGGCGGCTTAAATATGCTGAGCTAAG 471  
DB 182 ACAGCAGAGAAAGACAGGTTTGCATATGACACAGACAGCTCAACACTAGCTGTGATAC 241  
QY 472 GCTAGGCTTAATTTCTCATTTGA 496  
DB 242 GCAAGGCTTAATTTCTCGGACTTGA 266

## RESULT 14

US-09-640-211A-1872  
; Sequence 1872, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE REFERENCE: 11000.1021CIU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; LENGTH: 447  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-09-640-211A-1872

Query Match 9.1%; Score 72.2; DB 4; Length 447;  
Best Local Similarity 62.9%; Pred. No. 2.4e-11;  
Matches 129; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 292 GGTGTTCCGAGATTGGAACCGGTAAAGGGGCTTAGACGGGGCGCGGGGAAAGTTC 351  
DB 65 GGTATTGCAAGGCTCCGCAAGCTCTACAGAGGTGAGACAGAGGCACTGGGGGAAATGG 124  
QY 352 GCGCGGAGATTAAGGATCCGAAAAAGATCCAGATTGTTGGGTATACATACAG 411

Db 125 GTAGCAGAGATGCTATTACC---TAGAAATAGAACCCAGGCTGTGGCTTGAACTTTGAC 181  
QY 412 ACACCTGAGANGACACATTTGCTTATGATGACGCCGCTTAAATATGCGTGAAGCTAAA 471  
Db 182 ACAGCAGAGAGAGACACGCTTTGATATGACACAGCAGCCTACCACTAGTGTGAGTAC 241  
QY 472 GCTAGGCTTAATTTCTCATTTGA 496  
Db 242 GCAAGGCTTAATTTCCGACCTTGA 266

## RESULT 15

US-09-640-211A-436  
; Sequence 436, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE REFERENCE: 11000.102101U  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; CURRENT FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 436  
; LENGTH: 1775  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-09-640-211A-436

Query Match 9.1%; Score 71.8; DB 4; Length 1775;  
Best Local Similarity 58.2%; Pred. No. 6.8e-11;

Matches 146; Conservative 0; Mismatches 102; Indels 3; Gaps 1;

QY 242 GTGAGAGAGATTCGTGTGGGAAACCCGACAGAACGCGCGCGAGAGAGGTTGTCGA 301  
Db 513 GTTTCAGAGCTTCTTAGCTCGGGGCTTGTATGACCGCGGCCCAAGACGCGGTGAGAA 572  
QY 302 AGGATTGGAACCGGTATTAAGGCGCTTGAACGCGCGCGCTGCGGGAAGTTCCGCGCAGAA 361  
Db 573 AGAGGAAGATTTGTACAGAGGATCAGCCAACTCATGCGGGAATGGGCTGCAGAGA 632  
QY 362 TAGGATCCGAAAGAAAGAGATCCAGATTTGTTGGGTACATACGAGACCTGAGG 421  
Db 633 TCAGGAGTCCAGA--AAAGGCGCTAGGCTTGGCTGGTACCTTTAATACGCGCAGAG 689  
QY 422 ATGACGATTTGCTTATGATGACGCGCGCTTAAATATGCGTGAAGCTAAGCTAGGCTTA 481  
Db 690 AACCTGCTCGGCTTATGATGACGCTGCAGAAAGATCAGAGTAAAGAGCGGAAGTAA 749  
QY 482 ATTTTCTCAT 492  
Db 750 ATTTGTGAT 760

Search completed: March 7, 2005, 19:15:40  
Job time : 187 secs



Db 411 CGCGGAGATTGAGGATCCGAAGAAAGAGCTAGAGGTTTGCTCGGAGCTTACGAGA 470  
Qy 413 CACTGAGGATGACGATTTGCTTATGATGACCGCGCTTATATGCTGGAGCTAAG 472  
Db 471 CGCGGAGGACCGCGGGTGGCGTACGACCGCGCTTACGCTCAGAGATGGAAG 530  
Qy 473 CTAGGCTTAATTTTCTCATTTGATTGTTGTTGCAATATTTCCGAGCCGCTTAGAGTAAAC 532  
Db 531 CTAAAGCTGAATTTTCCGATTTGATTGTTCTTGAAGATAGACCGGTTAGATTAAGC 590  
Qy 533 CGAGAAACGTTTCCCTG 550  
Db 591 CTCGCCGTGCTCGCCGG 608

## RESULT 2

US-09-938-842A-2215  
Sequence 2215, Application US/09938842A  
Patent No. US20020160378A1  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
FILE REFERENCE: SRIPI300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 2215  
LENGTH: 681  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2215

Query Match 16.9%; Score 134; DB 9; Length 681;  
Best Local Similarity 63.8%; Pred. No. 4e-25;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 233 CGAAAGCTGTCAAGAGATTCTGTTGGGAACCCCGCAAGACCGCGCGGAGAG 292  
Db 191 CGGTACCTCTCCGGGAGGAAATTAAGCTTCCGCGCAGAAAGCGAGTGCCTCACAG 250  
Qy 293 GTTGTTCGAAGATTGGAACCGGTATTAAGGCGCTTAGACGCGCGCGTGGGGAAGTTG 352  
Db 251 CGCGGAGGCAAGAGGAGATGCACTACAGAGAGTGAAGAGGCGCGTGGGGAATTCG 310  
Qy 353 CGCGGAGATTAAGGATCCGAAAGAAAGATCCAGATTTGTTGGTATACATACGAGA 412  
Db 311 CGCGGAGATTGAGATCCGAAAGAAAGAGAGCTAGGTTTGGCTCGGAGATTACGAGA 370  
Qy 413 CACTGAGATGACGATTTGCTTATGATGACGCGCGCTTAAATATGCTGAGCTAAG 472  
Db 371 CGCGGAGGACGCGGCGTGGCGTACGACCGCGCTTTCAGCTCAGAGATGGAAG 430  
Qy 473 CTAGGCTTAATTTTCTCATTTGATTGTTGCAATATTTCCGAGCCGCTTAGAGTAAAC 532  
Db 431 CTAAAGCTGAATTTTCCGATTTGATTGTTCTTGAAGATAGACCGGTTAGATTAAGC 490  
Qy 533 CGAGAAACGTTTCCCTG 550  
Db 491 CTCGCCGTGCTCGCCGG 508

RESULT 3  
US-09-938-842A-2215

Sequence 2215, Application US/09938842A  
Publication No. US20040009476A9  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
FILE REFERENCE: SRIPI300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 2215  
LENGTH: 681  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2215

Query Match 16.9%; Score 134; DB 11; Length 681;  
Best Local Similarity 63.8%; Pred. No. 4e-25;  
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 233 CGAAAGCTGTCAAGAGATTCTGTTGGGAACCCCGCAAGACCGCGCGGAGAG 292  
Db 191 CGGTACCTCTCCGGGAGGAAATTAAGCTTCCGCGCAGAAAGCGAGTGCCTCACAG 250  
Qy 293 GTTGTTCGAAGATTGGAACCGGTATTAAGGCGCTTAGACGCGCGCGTGGGGAAGTTG 352  
Db 251 CGCGGAGGCAAGAGGAGTGAAGTACAGAGAGTGAAGAGGCGCGTGGGGAATTCG 310  
Qy 353 CGCGGAGATTAAGGATCCGAAAGAAAGATCCAGATTTGTTGGTATACATACGAGA 412  
Db 311 CGCGGAGATTGAGATCCGAAAGAAAGAGAGCTAGGTTTGGCTCGGAGCTTACGAGA 370  
Qy 413 CACTGAGATGACGATTTGCTTATGATGACGCGCGCTTAAATATGCTGAGCTAAG 472  
Db 371 CGCGGAGGACGCGGCGTGGCGTACGACCGCGCGCTTTCAGCTCAGAGATGGAAG 430  
Qy 473 CTAGGCTTAATTTTCTCATTTGATTGTTGCAATATTTCCGAGCCGCTTAGAGTAAAC 532  
Db 431 CTAAAGCTGAATTTTCCGATTTGATTGTTCTTGAAGATAGACCGGTTAGATTAAGC 490  
Qy 533 CGAGAAACGTTTCCCTG 550  
Db 491 CTCGCCGTGCTCGCCGG 508

## RESULT 4

US-09-770-149-325  
Sequence 325, Application US/09770149  
Patent No. US20020059663A1  
GENERAL INFORMATION:  
APPLICANT: Gorlach, Jörn  
APPLICANT: An, Yong-Qiang  
APPLICANT: Hamilton, Carol M.  
APPLICANT: Price, Jennifer L.  
APPLICANT: Raines, Tracy M.  
APPLICANT: Yu, Yang  
APPLICANT: Rameaka, Joshua G.  
APPLICANT: Page, Amy  
APPLICANT: Matthew, Abraham V.  
APPLICANT: Ledford, Brooke L.  
APPLICANT: Woessner, Jeffrey P.  
APPLICANT: Haas, William David  
APPLICANT: Garcia, Carlos A.  
APPLICANT: Krickler, Maya

```
/ APPLICANT: Slader, Ted
/ APPLICANT: Davis, Keith R.
/ APPLICANT: Allen, Keith
/ APPLICANT: Hoffman, Neil
/ APPLICANT: Hurban, Patrick
/ TITLE OF INVENTION: Expressed Sequences of Arabidopsis
/ FILE REFERENCE: 2024 (PARA-013PRV)
/ CURRENT APPLICATION NUMBER: US/09/770,149
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/178,506
/ PRIOR FILING DATE: 2000-01-27
/ NUMBER OF SEQ ID NOS: 999
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 325
/ LENGTH: 685
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-09-770-149-325
```

```
Query Match 16.9%; Score 134; DB 9; Length 685;
Best Local Similarity 63.8%; Pred. No. 4.1e-25;
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
```

```
QY 233 CGGAAGCTGTCTCAGAGATTCTGTGTGGAACCCCGCAGAGCGCGCGGAGAG 292
DB 73 CGCTTACCTCTCCGCGGAGGAAATTAAGCTCCGCGACGAGAGGAGTGCCTCACAG 132
QY 293 GTTGTTCGAAGATTGGAACCGGTATTAAGGCGCTTACGCGCGCGTGGGGAGTTGC 352
DB 133 CGCGGAGGAGGAGGAGATCAGTACAGAGATGAGAGAGAGCGCGTGGGGAAATTGC 192
QY 353 CGCGGAGATTAAGGATCCGAAAAGAAAGATCCAGATTTGTTGGTACATACAGAG 412
DB 193 CGCGGAGATTAAGGATCCGAAAAGAAAGATCCAGATTTGTTGGTACATACAGAG 252
QY 413 CACCTGAGATGAGATGCTTATGATGATGATGATGATGATGATGATGATGATGATG 472
DB 253 CGCGGAGATGAGATGCTTATGATGATGATGATGATGATGATGATGATGATGATG 312
QY 473 CTAGGCTTAATTTCTCTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 532
DB 313 CTAGGCTTAATTTCTCTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 372
QY 533 CGAGAAACGTTTCCTG 550
DB 373 CTCGCCGTGCTCGCCG 390
```

## RESULT 5

```
US-10-225-068-127
/ Sequence 127, Application US/10225068
/ Publication No. US20030217383A1
/ GENERAL INFORMATION:
/ APPLICANT: Mendel Biotechnology, Inc.
/ APPLICANT: Reuber, T. Lynne
/ APPLICANT: Riechmann, Jose Luis
/ APPLICANT: Heard, Jacqueline E.
/ APPLICANT: Jiang, Cai-Zhong
/ APPLICANT: Adam, Luc J.
/ APPLICANT: Dubell, Arnold T.
/ APPLICANT: Ratcliffe, Oliver
/ APPLICANT: Pineda, Omaira
/ APPLICANT: Yu, Guo-Liang
/ APPLICANT: Broun, Pierre E.
/ TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
/ TITLE OF INVENTION: POLYPEPTIDES IN PLANTS
/ FILE REFERENCE: 514442002040
/ CURRENT APPLICATION NUMBER: US/10/225,068
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: 60/310,847
/ PRIOR FILING DATE: 2001-08-09
/ PRIOR APPLICATION NUMBER: 60/336,049
```

```
/ PRIOR FILING DATE: 2001-11-19
/ PRIOR APPLICATION NUMBER: 60/338,692
/ PRIOR FILING DATE: 2001-12-11
/ PRIOR APPLICATION NUMBER: 10/171,468
/ PRIOR FILING DATE: 2002-06-14
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 127
/ LENGTH: 913
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (81)...(761)
US-10-225-068-127
```

```
Query Match 16.9%; Score 134; DB 17; Length 913;
Best Local Similarity 63.8%; Pred. No. 4.7e-25;
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
```

```
QY 233 CGGAAGCTGTCTCAGAGATTCTGTGTGGAACCCCGCAGAGCGCGCGGAGAG 292
DB 271 CGCTTACCTCTCCGCGGAGGAAATTAAGCTCCGCGACGAGAGGAGTGCCTCACAG 330
QY 293 GTTGTTCGAAGATTGGAACCGGTATTAAGGCGCTTACGCGCGCGTGGGGAGTTGC 352
DB 331 CGCGGAGGAGGAGGAGATCAGTACAGAGATGAGAGAGAGCGCGTGGGGAAATTGC 390
QY 353 CGCGGAGATTAAGGATCCGAAAAGAAAGATCCAGATTTGTTGGTACATACAGAG 412
DB 391 CGCGGAGATTAAGGATCCGAAAAGAAAGATCCAGATTTGTTGGTACATACAGAG 450
QY 413 CACCTGAGATGAGATGCTTATGATGATGATGATGATGATGATGATGATGATGATG 472
DB 451 CGCGGAGGAGCGCGGCGTGGCGTACGACCGCGCGCTTACGCTCAGAGATCCAAA 510
QY 473 CTAGGCTTAATTTCTCTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 532
DB 511 CTAGGCTTAATTTCTCTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 570
QY 533 CGAGAAACGTTTCCTG 550
DB 571 CTCGCCGTGCTCGCCG 588
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## RESULT 6

```
US-10-374-780A-5
/ Sequence 5, Application US/10374780A
/ Publication No. US20040019927A1
/ GENERAL INFORMATION:
/ APPLICANT: Sherman, Bradley K
/ APPLICANT: Riechmann, Jose Luis
/ APPLICANT: Jiang, Cai-Zhong
/ APPLICANT: Heard, Jacqueline E
/ APPLICANT: Haake, Volker
/ APPLICANT: Creelman, Robert A
/ APPLICANT: Ratcliffe, Oliver
/ APPLICANT: Adam, Luc J
/ APPLICANT: Reuber, T. Lynne
/ APPLICANT: Keddie, James
/ APPLICANT: Broun, Pierre E
/ APPLICANT: Pilgrim, Marsha L
/ APPLICANT: Dubell III, Arnold T
/ APPLICANT: Pineda, Omaira
/ APPLICANT: Yu, Guo-Liang
/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
/ FILE REFERENCE: MRI-0047 CIP
/ CURRENT APPLICATION NUMBER: US/10/374,780A
/ PRIOR FILING DATE: 2003-02-25
/ PRIOR APPLICATION NUMBER: 09/837,944
/ PRIOR FILING DATE: 2001-04-18
/ PRIOR APPLICATION NUMBER: 60/310,847
/ PRIOR FILING DATE: 2001-08-09
```

```

; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 913
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G22
US-10-374-780A-5

```

```

Query Match      16.9%; Score 134; DB 17; Length 913;
Best Local Similarity 63.8%; Pred. No. 4,7e-25;
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

```

```

QY 233 CGGAAAGCTGTGACGAGATTTCTGTTGGGAAACCCCGGCAAGAGCGCGCGGAGAG 292
DB 271 CGGTTACCTCTCCGGCGGAGGAAATTAAGCTCTCCGCGCAAGAGCGAGTGGCTCACAG 330
QY 293 GTTGTTCGAGGATTGGAACCGGTATTAAGGCGCTTAGACGCGCGCGGTGGGAAAGTTG 352
DB 331 CGCCGAGGAGAGAGGAGATGACGTACAGAGAGTACAGAGAGCGCGGTGGGAAATTCG 390
QY 353 CGGCGAGATTAAGGAGATCCGAAAGAAAGATCCAGAGATTTGTTGGGTACATACGAGA 412
DB 391 CGGCGAGATTAAGGAGATCCGAAAGAAAGATCCAGAGATTTGTTGGGTACATACGAGA 450
QY 413 CACCTGAGAGATGACGATTTGCTTATGATGACCGCGCTTTAATTTGCTGAGAGTAAAG 472
DB 451 CGCCGAGGAGAGCGGGGGGTGACGACCGAGCGCGCTTCAAGCTCAGAGAGATCGAAG 510
QY 473 CTAGGCTTAATTTCTCATTTGATTGTTGATTAATTTCCGAGACCGCTTAGAGTAAAC 532
DB 511 CTAGGCTGAATTTCCGCAATTTGATTGTTGTTGTAAGTATGAGCGGTTAGATTAGGC 570
QY 533 CGAGAAACGTTTCCTG 550
DB 571 CTCGCCGTGCTCGCCGG 588

```

# RESULT 7

```

US-10-412-699B-27
; Sequence 27, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Broun, Pierre E.
; APPLICANT: Pineda, Omlia
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.

```

```

; APPLICANT: Dubell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kimimoto, Roderick
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142
; PRIOR FILING DATE: 2001-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 913
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G22
US-10-412-699B-27

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Query Match      16.9%; Score 134; DB 17; Length 913;
Best Local Similarity 63.8%; Pred. No. 4,7e-25;
Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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QY 233 CGGAAAGCTGTGACGAGATTTCTGTTGGGAAACCCCGGCAAGAGCGCGCGGAGAG 292
DB 271 CGGTTACCTCTCCGGCGGAGGAAATTAAGCTCTCCGCGCAAGAGCGAGTGGCTCACAG 330
QY 293 GTTGTTCGAGGATTGGAACCGGTATTAAGGCGCTTAGACGCGCGCGGTGGGAAAGTTG 352
DB 331 CGCCGAGGAGAGAGGAGATGACGTACAGAGAGTACAGAGAGCGCGGTGGGAAATTCG 390
QY 353 CGGCGAGATTAAGGAGATCCGAAAGAAAGATCCAGAGATTTGTTGGGTACATACGAGA 412
DB 391 CGGCGAGATTAAGGAGATCCGAAAGAAAGATCCAGAGATTTGTTGGGTACATACGAGA 450
QY 413 CACCTGAGAGATGACGATTTGCTTATGATGACCGCGCTTTAATTTGCTGAGAGTAAAG 472
DB 451 CGCCGAGGAGAGCGGGGGGTGACGACCGAGCGCGCTTCAAGCTCAGAGAGATCGAAG 510
QY 473 CTAGGCTTAATTTCTCATTTGATTGTTGATTAATTTCCGAGACCGCTTAGAGTAAAC 532
DB 511 CTAGGCTGAATTTCCGCAATTTGATTGTTGTTGTAAGTATGAGCGGTTAGATTAGGC 570
QY 533 CGAGAAACGTTTCCTG 550
DB 571 CTCGCCGTGCTCGCCGG 588

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# RESULT 8

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US-09-777-207-1
; Sequence 1, Application US/09777207
; Publication No. US20020039780A1
; GENERAL INFORMATION:

```



```

; APPLICANT: Horvath, Diana M.
; APPLICANT: Chua, Nam-Hai
; APPLICANT: Stuijver, Maarten H.
; APPLICANT: Jepsen, Ian
; TITLE OF INVENTION: New Salicylic Acid Inducible Genes and Promoters
; FILE REFERENCE: PB/5-50067A
; CURRENT APPLICATION NUMBER: US/09/777,207
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US60/095,187
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-777-207-1

Query Match          16.3%; Score 129.4; DB 9; Length 708;
Best Local Similarity 64.2%; Pred. No. 6,9e-24;
Matches 210; Conservative 0; Mismatches 116; Indels 1; Gaps 1;

QY 245 AGGAGATTCTGTGTGGGAGACCCCGCAGAGCGCGCGGAGAGAGTTGTTGCAAG 304
    |||||
DB 145 AGGAGAAATTGTGTCTCCAGCGATACACGCGCGCGCGGCTGAGTTACCGA 204

QY 305 ATTGGAACCGGTATAGCGCGTTAGACGCGCGCGCGGAGAGTTGCGCGCGAGTAA 364
    |||||
DB 205 GGGGAGGAGATTACAGAGGTTAGACGAGCGCTTGGGGGAAATTTGGCGCGAGATT 264

QY 365 GGGATCCGAAAAAGAAAGATCCA-GGATTTGGTGGGTACATACAGACACCTCGAGGAT 423
    |||||
DB 265 GGGATCCGCGGAGAAATGAGCTAGAGTTTGGCTTGGAAACATACAGAAAGATGAAGT 324

QY 424 GGAGATTGGCTTATGATGAGCGCGGTTTAAATATGCGTGAAGCTAAGCTTAGCTTAAT 483
    |||||
DB 325 GCTGCAATGCTTATGATTAAGCGGCTTATAGATGATGTTCAAGGCTCATTTAAAT 384

QY 484 TTTCCTCATTTGATTGGTTCGAATATTTCCGAGCCGCTTAGATTAACCGAGAAAAGCT 543
    |||||
DB 385 TTTCACATAGAGTCGTTTAAATGAACCGGAAACCGTTGAGGTACGGGAGAAAAGCGA 444

QY 544 TTCCCTGCGGAGCCTTCTACGAGCTCG 570
    |||||
DB 445 GCCTCCCTGAGACCGGCTAGTCTGTCG 471

RESULT 9
US-10-341-961A-193
; Sequence 193, Application US/10341961A
; Publication No. US20040006787A1
; GENERAL INFORMATION:
; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
; APPLICANT: Curagen Corporation
; APPLICANT: Crasera, Oswald
; APPLICANT: Swireky, Peter
; APPLICANT: Mysore, Kiran
; APPLICANT: Folkerts, Otto
; APPLICANT: Martin, Gregory
; APPLICANT: Ekengren, Sophia
; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOC
; TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE
; FILE REFERENCE: BTI 67A2
; CURRENT APPLICATION NUMBER: US/10/341,961A
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: 60390249
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60261029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60348792
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 193
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-341-961A-193

Query Match          16.2%; Score 128.6; DB 17; Length 437;
Best Local Similarity 69.0%; Pred. No. 8.8e-24;
Matches 176; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 316 TATAGAGCGCTTAGACGCGCGCGTGGGAGAGTTGCGCGGAGATTAAGGATCCGAAA 375
    |||||
DB 10 TATAGAGCGCTTAGACGCGCGCGTGGGAGAGTTGCGCGGAGATTAAGGATCCGCGC 69

QY 376 AAGAAAGATCCAGGATTTGGTGGTACATACGACACCTAGAGATGAGATTTGGCT 435
    |||||
DB 70 AAGAACGAGCTAGAGGTTGGCTTGGAAAGTAAAGTAAAGCTGCAATTTGCT 129

QY 436 TATGATGACGCGCGCTTATATATGCGTGAAGCTAAGCTTAAGCTTAATTTCCCATTTG 495
    |||||
DB 130 TATGATTAAGCTGCTTATAGATGAGAGATCAAAAGCATTTGAAATTTCCGACCGG 189

QY 496 ATTGTTGCAATATTTCCGAGCCGCTTAGAGTAAACCGAGAAACGTTTCCCTGCGAG 555
    |||||
DB 190 ATCGTTTGAATGAACCGGACCGGTTGAGTTACGCGGAAAGCGAGCATGCGCGAA 249

QY 556 CCTTCTACGAGCTCG 570
    |||||
DB 250 CCGCAAGCTCTGTCG 264

RESULT 10
US-10-425-114-29849
; Sequence 29849, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 29849
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-GMROPIC008H09_FLI
US-10-425-114-29849

Query Match          14.9%; Score 118.2; DB 17; Length 995;
Best Local Similarity 72.5%; Pred. No. 8e-21;
Matches 153; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 297 TTGGAAGATTGGAACCGGTTATTAAGCGGCTTGAACGCGCGCGTGGGAGAGTTCCGCGC 356
    |||||
DB 390 TCCAAAGAGGGGTGAGCTACCGAGCGTGCAGAGAGCGCGTGGGAGAGTATCGCGC 449

QY 357 GAGATTAAGGATCCGAAAAAGAAAGATCCAGATTTGGTGGTATACGAGACACC 416
    |||||
DB 450 GAGATTAAGGACATTAAGAGAGATGTGAGAGTGTGGCTTGGAACTTACGAAACCGC 509

QY 417 TGAGATGAGCATTTGGCTTATGATGACACCGCGTTTATATGCGTGAAGCTTAAGCTAG 476
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DB 510 TGAGATGAGCATTTAGCTTATGATGACACCTCATTTAAGATGCGGCGCTCAAAAGCTAA 569

QY 477 GCTTAATTTTCTCATTTGATTGTTGCAAT 507
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; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142
; PRIOR FILING DATE: 2001-03-27
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 978
; LENGTH: 1049
; TYPE: DNA
; ORGANISM: Glycine max
US-10-412-699B-978
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Query Match 14.8%; Score 118.2; DB 17; Length 1049;
Best Local Similarity 72.5%; Pred. No. 8.2e-21;
Matches 153; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
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QY 297 TTGAAGATTGACCGGTATTAAGCGCGTTCAGCGCGCGCGGGAAGTTCCGGCG 356
DB 649 TCAGAAAGAGGGTTGAGCTACCGAGCGCTGCGAGAGCGCTGGGGAAGTATGCGCG 550
QY 357 GGAAGATTAAGGATCCGAAAAAAGAGATCCAGATTGGTTGGGTACATACGACACC 416
DB 589 GGAGATTAGGACACTAAGAGAGATGCTGAGAGTGTGCTTGAACCTACGAAACCGC 530
QY 417 TAGAGTGAAGCATTTGGCTTATATGACCGCGCTTAAATATGCTGAGCTAAAGCTAG 476
DB 529 TAGAGATGAGCTTGTAGCTTATATGATCGAGCTGCAATTTAAGATCGGGGCTCAAAAGCTAA 470
QY 477 GCTTAATTTCTCATTTGATTTGCTGCAAT 507
DB 469 GCTGAATTTCTCATTTAATTTGCTGCAAT 439

RESULT 14
US-10-122-822-4
; Sequence 4, Application US/10122822
; Publication No. US20030084477A1
; GENERAL INFORMATION:
; APPLICANT: Purdue Research Foundation
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: 7024-511
; CURRENT APPLICATION NUMBER: US/10/122,822
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/202,161
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: PCT/US97/10382
; PRIOR FILING DATE: 1997-06-12
; PRIOR APPLICATION NUMBER: 60/046,494
; PRIOR FILING DATE: 1997-05-14
; PRIOR APPLICATION NUMBER: 60/019,633
; PRIOR FILING DATE: 1996-06-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: ASCII
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; SEQ ID NO 4
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-122-822-4
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Query Match 14.7%; Score 116.2; DB 14; Length 933;
Best Local Similarity 67.8%; Pred. No. 2.6e-20;
Matches 177; Conservative 0; Mismatches 83; Indels 1; Gaps 1;
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QY 278 CGGCGCCCGGAGGAGTGTTCGAGAGATTGAAACCGGTATTAAGGCGCTTAAAGCGCGC 337
DB 312 CGGCAAGCTCCGCGCGCTGAACAACGAAAAAGACATTATTAAGCGCTTAAAGCGCGCTC 371
QY 338 CGTGGGGGGAAGTCCGGGGCGGAGATTAAGGATCCGAAAAAGATCCAGATTGCT 397
DB 372 CGTGGGGGGAATTTGGCGGAGATTGAGATCCGCGAAGACGAGCTTAAGGCTTTGGC 431
QY 398 TGGGTACATACGACACCTGAGATGACGATTTGCTTATGATGACGCGCTTTAATA 457
DB 432 TTGAAACGTACGAAACGCTGAGAGAGCTGCAATTCCTTATGATTAAGCTTTATAGAA 491
QY 458 TGGGTGAGCTAAAGCTTAAGCTTAATTTCTCATTTGATTTGTTGCAATATTTCCGAC 517
DB 492 TGAGAGATCAAAAGACATTTGAATTTCCGACCGATCGTTGAAT-GAACCGGAA 550
QY 518 CGCTTAGAGTAAACCGGAGAA 538
DB 551 CGCTTAGAGTAAACCGGAGAA 571
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## RESULT 15

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US-10-739-930-3666
; Sequence 3666, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kowalcik, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 3666
; LENGTH: 809
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: GLVMA-23APR03-CLUSTER5319_2
US-10-739-930-3666
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Query Match 14.6%; Score 115.4; DB 18; Length 809;
Best Local Similarity 74.1%; Pred. No. 4e-20;
Matches 146; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
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QY 307 TGAACCGGTATTAAGCGCTTGAAGCGCGCGTGGGGGAAGTTCCGCGCGGATTAAG 366
DB 296 TGAACCGGTATTAAGCGCGCGCTGAAGCGCTGACCTTGGGGCAAGTTCCGCGCGGAAATAGA 355
QY 367 GATCCGAAAAAAGAAAGATCCAGATTGTTGGGTACATTAAGAGACCTGAGATGCA 426
DB 356 GATCCGAAAAAAGAAAGATGCTGAGATGCTTGGGACTTAAGAACTGAGAGAAAGCG 415
QY 427 GCAATGCTTATGATGACCGCGGTATTAATATGCTGAGACTTAAGCTTAAGCTTAATTT 486
DB 416 GGTATGCTTATGATGAGCTGCTTTAAGATGCGTGGCAGAAAGCTAAGTAAATTTT 475
QY 487 CCTCATTTGATTGCTTC 503
DB 476 CTTCACTCATTTGCTTC 492
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Search completed: March 7, 2005, 20:36:10

Tue Mar 8 08:51:45 2005

us-09-890-782-3.rnpb

Page 8

Job time : 599 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 16:48:09 ; Search time 3384 Seconds  
(without alignments)  
8908.653 Million cell updates/sec

Title: US-09-890-782-3

Perfect score: 792  
Sequence: 1 ttcttaaaagaagaagaataa.....ttatcccaaaaagttcac 792

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hnc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	161	20.3	605	7	CK715561 LERSF01B0
2	154.6	19.5	944	7	CN385373 LERTR03G2
3	153	19.3	673	7	CN385772 LERTR0410
4	152.4	19.2	760	7	CK936905 CGF100451
5	134	16.9	903	3	CNS0A088X Arabidops
6	133	16.8	563	1	AV552445 AV552445
7	133	16.8	531	2	BE449392 EST336151
8	133	16.8	663	1	AV822925 AV822925
9	132.8	16.8	490	6	CA520877 KS11018B1
10	132.6	16.7	636	6	CB078370 h166g10.9
11	130.2	16.4	903	2	BF275652 GA_EB002
12	129.8	16.4	652	4	BG128566 EST747212
13	128.6	16.2	437	1	AT771213 EST252409
14	128.2	16.2	575	2	AM034216 EST277787
15	128	16.2	638	2	AM584731 N210846e
16	128	16.2	643	2	AM980654 EST391807
17	128	16.2	705	4	BG587407 EST489179
18	128	16.2	707	4	BG647799 EST509418
19	128	16.2	798	6	CA922634 EST640352
20	127.6	16.1	930	7	CK288039 EST730761
21	126.6	16.0	585	7	CF090946 QHM6J15.Y
22	126	15.9	842	7	CK276642 EST722720
23	126	15.9	870	7	CK258279 EST741916
C 24	125.4	15.8	775	7	CK278893 EST724971

C 25	125.4	15.8	805	7	CN214825	CN214825 28570 Sus
26	125.4	15.8	857	7	CK278892	CK278892 EST724970
27	125.4	15.8	946	7	CK277725	CK277725 EST723803
28	125	15.8	703	7	CF088650	CF088650 QHM1118.Y
C 29	124.4	15.7	739	6	CK258280	CK258280 EST741917
C 30	124.4	15.7	739	6	CA920051	CA920051 EST637769
C 31	123.8	15.6	809	6	CD574882	CD574882 UCRPT01.0
C 32	123.4	15.6	622	5	BO517083	BO517083 EST624458
C 33	123.4	15.6	652	5	BO517082	BO517082 EST624497
34	123.4	15.6	696	7	CF091941	CF091941 QHM9009.Y
35	123.4	15.6	841	5	BQ047502	BQ047502 EST596620
C 36	123.4	15.6	949	7	CK268018	CK268018 EST714096
C 37	123.4	15.6	980	7	CK268019	CK268019 EST714097
C 38	122.8	15.5	687	4	BG584897	BG584897 EST486659
39	122.8	15.5	794	6	CF069648	CF069648 EST670369
40	122.8	15.5	818	4	BG582281	BG582281 EST484022
C 41	122.6	15.5	774	7	CO112337	CO112337 GR_EB004
42	122.6	15.5	780	7	CO1123742	CO1123742 GR_EB004
43	122.6	15.5	843	7	CO112338	CO112338 GR_EB004
44	122.2	15.4	578	7	CF507919	CF507919 USDA-PP.1
45	122	15.4	544	4	BI921995	BI921995 EST541858

## ALIGNMENTS

RESULT 1  
CK715561/c  
LOCUS  
DEFINITION  
CK715561 LERSF01B02 Subtractive cDNA library prepared from tomato infected with Ralstonia solanacearum (Rs-CK) Lycopersicon esculentum cDNA clone LERSF01B02, mRNA sequence.

ACCESSION  
CK715561  
VERSION  
CK715561.1 GI:50879390  
KEYWORDS  
EST.  
SOURCE  
Lycopersicon esculentum (tomato)  
ORGANISM  
Lycopersicon esculentum

REFERENCE  
AUTHORS  
TITLE  
Liu, W.C., Cheng, M.L., Ting, H.M. and Cheng, C.P.  
Functional genomics study of tomato genes responsive to bacterial wilt

JOURNAL  
COMMENT  
Unpublished (2004)  
Contact: Chiu-Ping Cheng  
Crop Plant Improvement Group  
Institute of Bioagricultural Sciences, Academia Sinica  
Nankang, Taipei, 115, Taiwan, Republic of China  
Tel: 886-2-2652-2268  
Fax: 886-2-2561-5600  
Email: chiuping@gate.sinica.edu.tw  
Insert Length: 605 Std Error: 0.00  
Plate: 01 row: B column: 02  
Seq primer: Spc.

FEATURES  
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Location/Qualifiers  
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/cui="taxon:4081"  
/db\_xref="taxon:4081"  
/clone="LERSF01B02"  
/feature\_type="root and collar"  
/dev\_stage="Three weeks old"  
/lab\_host="Xil-Blue"  
/clone\_lib="Subtractive cDNA library prepared from tomato infected with Ralstonia solanacearum (Rs-CK)"  
/note="Vector: pGEM-T-EZ; Plant samples were provided by Dr. Jaw-Fen Wang (Taiwan, AVRDC). Each plant grown in a 3-inch pot was inoculated with 30 ml (108cfu/ml) of Rs strain Pas4 to give a final concentration of 108cfu/g soil. Roots and collars of inoculated and control plants were harvested 24 and 48 hours post inoculation (e.g.

## ORIGIN

24-control, 24-inoculated, 48-control and 48-inoculated). Poly(A) RNA was purified from total RNA specimen isolated from individual samples. The poly(A) RNA specimen prepared from 24-control and 48-control samples were mixed at 1:1 ratio. The poly(A) RNA specimen prepared from 24-inoculated and 48-inoculated samples were also mixed at 1:1 ratio. Tomato cDNA library LERSF was then constructed by subtracting the pooled control specimen from the pooled inoculated specimen using ClontechPCR-select cDNA Subtraction kit."

Query Match 20.3%; Score 161; DB 7; Length 605;  
Best Local Similarity 73.3%; Pred. No. 1.8e-31;  
Matches 206; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 304 GATTGAAACCGGTATTAAGGCGCTTAGACGCGCGCGTGGGGAAGTTCCGCGCGAATA 363  
DB 343 GATTGAAACCGGTATTAAGGCGCTTAGACGCGCGCGTGGGGAAGTTCCGCGCGAATA 284  
QY 364 AGGATCCGAAAAAGAAAGATTCAGGATTTGGTGGTACATACGAGACACCTGAGGAT 423  
DB 283 AGAGACCCCGATAGAAAGAGTGTCTAGGCTTTGGCTAGGACTTACGAGACCTGAGAT 224  
QY 424 GAGCATTTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483  
DB 223 GAGCATTTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 164  
QY 484 TTTTCTCATTTGATTTGTTGCAATATTTCCGAGCCCGTAAAGTAAACCCGAGAAAGT 543  
DB 163 TTTTCTCATTTGATTTGTTGCAATATTTCCGAGCCCGTAAAGTAAACCCGAGAAAGT 104  
QY 544 TTTCCCTGAGAGCGCTTCTACAGAGTGTGCTGCTTCTTCTTC 584  
DB 103 TGCCACTCGTACAGTATCATTTGTAATATTAACCTTTC 63

RESULT 2  
CN385373 944 bp mRNA linear EST 31-AUG-2004  
LOCUS LE2TR03624 Tomato CL5915 roots under different developmental stages  
DEFINITION Lycopersicon esculentum cDNA clone LE2TR03624, mRNA sequence.  
ACCESSION CN385373  
VERSION CN385373.1 GI:51700687  
KEYWORDS EST.  
SOURCE Lycopersicon esculentum (tomato)  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 944)  
Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.  
DNA microarray profiling of gene expression during tomato root development  
TITLE Unpublished (2004)  
JOURNAL Contact: Kin-Ying, To  
COMMENT Crop Plant Improvement Group  
Institute of Biagricultural Sciences, Academia Sinica  
128 Academia Rd, Section 2, Taipei, Taiwan 11529  
Tel: 886-2-2653-3161  
Fax: 886-2-2653-5600  
Email: kyto@gate.sinica.edu.tw  
Insert Length: 944 Std Error: 0.00  
Plate: 03 row: G column: 24  
Seq primer: smart2.

FEATURES  
source Location/Qualifiers  
1..944

/organism="Lycopersicon esculentum"  
/mol\_type="mRNA"  
/culivar="CL5915"  
/db\_xref="taxon:4081"  
/clone="LE2TR03624"  
/issue\_type="roots"

## ORIGIN

/dev\_stage="1-, 2-, 3-, and 4- month-old"  
/lab\_host="E.coli BM25.8"  
/clone\_lib="Tomato CL5915 roots under different developmental stages"  
/note="Vector: pT7E2; Tomato CL5915 seeds are obtained from AVRDC. Roots were harvested from plants grown under different developmental stages: 1-, 2-, 3-, 4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA Library construction kit, Clontech)"

Query Match 19.5%; Score 154.6; DB 7; Length 944;  
Best Local Similarity 70.0%; Pred. No. 9.9e-30;  
Matches 208; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 256 GTTGTGGAAACCCCGCAGAAAGCGCGCGGAGAGGTTTCCAGAGATTGGAACCGG 315  
DB 229 GTTGAAGAGTCCAGACAGTGTGGCAAGTGTGAAACAGCACCAAAAGATTGGAAGCGG 288  
QY 316 TATAAGGCGCTTAGACGCGCGCGTGGGGAAGTTCCGCGCGAGATAAGATCCGAA 375  
DB 289 TACCGAGAGTAAAGAGAGCGCGTGGGTAATTTCCGCGAGATAAGATCCGAA 348  
QY 376 AAGAAAGATCCAGATTTGTTGGGTACATACAGACACCTGAGATGACGATTTGCT 435  
DB 349 AAGAAAGATCCAGATTTGTTGGGTACATACAGACACCTGAGATGACGATTTGCT 408  
QY 436 TATGATGACAGCCCGTTTAAATAGCTGAGAGCTAAAGCTTAATTTTCTCATTTG 495  
DB 409 TATGACCAAGCCCGATTCAGATTTGCTGCTCAAAAGCTAAGCTTAATTTTCTCATTTA 468  
QY 496 ATTGTTGCAATTTTCCGAGCCGTTAAGTAAACCCGAGAAAGCTTTCCTGCG 552  
DB 469 ATGCGCTCGGCTGTCCCGAGCCGCTAAGGTGAACCTTAAGGCTGATCGCATTTG 525

RESULT 3  
CN385772 673 bp mRNA linear EST 31-AUG-2004  
LOCUS LE2TR04102 Tomato CL5915 roots under different developmental stages  
DEFINITION Lycopersicon esculentum cDNA clone LE2TR04102, mRNA sequence.  
ACCESSION CN385772  
VERSION CN385772.1 GI:51701086  
KEYWORDS EST.  
SOURCE Lycopersicon esculentum (tomato)  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 673)  
Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.  
DNA microarray profiling of gene expression during tomato root development  
TITLE Unpublished (2004)  
JOURNAL Contact: Kin-Ying, To  
COMMENT Crop Plant Improvement Group  
Institute of Biagricultural Sciences, Academia Sinica  
128 Academia Rd, Section 2, Taipei, Taiwan 11529  
Tel: 886-2-2653-3161  
Fax: 886-2-2653-5600  
Email: kyto@gate.sinica.edu.tw  
Insert Length: 673 Std Error: 0.00  
Plate: 04 row: I column: 02  
Seq primer: smart2.

FEATURES  
source Location/Qualifiers  
1..673

/organism="Lycopersicon esculentum"  
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/culivar="CL5915"  
/db\_xref="taxon:4081"  
/clone="LE2TR04102"  
/issue\_type="roots"

/dev stage="1-2-3", and 4 - month-old"  
/lab host="E.coli BM25.8"  
/clone lib="Tomato CL5915 roots under different developmental stages"  
/note="Vector: pTriplex2; Tomato CL5915 seeds are obtained from AVRDC. Roots were harvested from plants grown under different developmental stages: 1-2-3-4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA Library construction kit, Clontech)"

## ORIGIN

Query Match 19.3%; Score 153; DB 7; Length 673;

Best Local Similarity 69.7%; Pred. No. 2.5e-29; Indels 0; Gaps 0;

Matches 207; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

256 GTTGTGGGAACCCCGCAGAGCGCGCGAGGAGTGTTCGAAGATTGGAACCG 315

193 GTTGAAGAGTCCGAGACAGTGTGCAAGTGAACACGACCAAAAGATTGGAACCG 252

316 TATAGGCGGTTAGACGCGCGCGGTGGGAGATTGCGCGGAGATTAAGGATCCGAA 375

253 TACCGAGAGTAAAGAGAGCGCGGTGGGTAATTCGCGCGAGATTAAGGATCCGAT 312

376 AAGAAAGATCCAGATTGTTGGTATCAATAGACACCTAGAGATGAGCATTTGGCT 435

313 AAAAAAATGCGAGTTATGTATGAGACTTATGAGACACCGAGATGAGCATTTGGCT 372

436 TATGATGACGCGCGGTTATATGCGTGAAGCTAAGCTAATTTCTCATTTG 495

373 TATGACCAAGCCGATTCAGATTCTGTGCTCGAAAGCTAATTTCTCATTTA 432

496 ATTGTTGCAATATTTCCGACCGCGTGAAGTAACCGGAAACGTTTCCCTGCG 552

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

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433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

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433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

433 ATCGGCTCGGCTGTCCCGAGCGCGCTAGAGTGAACCTAGCGTGCATTCG 489

/lab host="XL10-Gold"  
/clone lib="Developing fruit Flavado at 80 DAFB"  
/note="Torgan: Fruit; Vector: pTriplex2; Site 1: SL1A; Site 2: SL1B; Developing citrus fruits were harvested from trees growing in the 'Citrus variety collection' in the Wolfskill experimental orchard located in Winters, California (USA). Fruit was collected on July 29, 2003, between 8 to 9 am and stored at 4°C. The flavado tissue was dissected out of developing fruit (80 DAFB) and used to isolate RNA using Trizol reagent from Invitrogen. The cDNA library was constructed using the SMART cDNA library kit (Clontech). The primary library was en masse evicted and plasmid DNA containing the cDNA library was isolated from the resultant bacterial population. Plasmid DNA was then transformed into ultra competent E. coli cells (XL10 Gold; Stratagene). Transformants were plated out on Q-trays (2000 cfu/tray), picked using a Qbot and archived in 384 well dishes."

## ORIGIN

Query Match 19.2%; Score 152.4; DB 7; Length 760;

Best Local Similarity 67.8%; Pred. No. 3.6e-29; Indels 0; Gaps 0;

Matches 213; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

282 GGCCGAGGAGGTTGTCGAGGATTCGAACCGGTATAGGCGGCTAGACGCGCGCTG 341

278 GATGTGCGACGTTGAGTCACTGAGTGAAGTGAAGCGCTGAGAGGCGCTG 337

342 GGGGAAGTTGCGGCGGAGATTAAGGATCCGAAAGAAAGATCCAGATTGTTGGG 401

338 GGGGAAGTTGCTGCGGAGATTAAGGACCTTAAGAAAGATGGGGCAAGATTGGCTGG 397

402 TACATGACGACACTGAGAGTCAAGTTCGTTATGATCAAGCCGCTTAAATATGCG 461

398 CACCTATGATACCCCGAGGCTGACATTTCTTATGATGAGCCGCTTCAAGATGCG 457

462 TGGAGTAAAGTAGGCTTAATTTCCATTTGATGTTGATGATTTCCGAGACCGGT 521

458 AGGCTCAAGGCTTAAGCTCAATTTCTCACTGATGCTCAATGTTGAGCCCGGT 517

522 TAGATTAACCGGAGAAAGTTCCTCGGAGCCCTTACGACCTGCTGCTTCTTC 581

518 TAGGTTACCAAGAACCGGCTTCCCAAGCCTCCTCTTCTGCTTCTTCTTC 577

582 TTCTTCTGCTG 595

578 ATCATCATCCGTTG 591

578 ATCATCATCCGTTG 591

578 ATCATCATCCGTTG 591

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578 ATCATCATCCGTTG 591

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578 ATCATCATCCGTTG 591

578 ATCATCATCCGTTG 591

**TITLE** Direct Submission  
**JOURNAL** Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)

**COMMENT** - Web : www.genoscope.cns.fr  
 The sequences are based on single pass reads.  
 Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.  
 Genoscope members carried out sequencing and annotation : Castel I V., Aury J.M., Jallion O., Winkler P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.  
 URGV INRA : Clepet C., Caboche M.  
 Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information Center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.  
[http://www.genoscope.cns.fr/externe/sequences/Banque\\_Projet\\_EF/Full\\_length](http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length)  
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.

**FEATURES**  
 source  
 location/Qualifiers  
 1..903  
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 /mol\_type="mRNA"  
 /strain="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="GSLR51U772E09"  
 /issue\_type="Siliques"  
 /plasmid="pCMVSPORT\_6"  
 1..903  
 /gene="At2g44840"

**ORIGIN**

Query Match 16.8%; Score 134; DB 3; Length 903;  
 Best Local Similarity 63.8%; Pred. No. 2.8e-24;  
 Matches 203; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 233 CGAAGCTGTCAAGAGATTCTGTGTGGAAACCCGCCAAGACCGCGCCGAGAG 292  
 Db 276 CCGTACCTCTCCGGGAGGAAATPAACCTCCGCGACGAAGCGAGTGCACAG 335  
 QY 293 GTTGTTCGAAGATTGGAACCGGTATAGGGCGTTAGACGCGCGCGTGGGGAAGTTG 352  
 Db 336 CGCCGAGGCAAGAGGGAGTGCAGTACAGAGAGTGAAGAGCGCCGTGGGGAATTG 395  
 QY 353 CGCGGAGATPAAGGATCCGAAAAAGAAAGATCCAGATTGTGGTACATACAGA 412  
 Db 396 CGCGGAGATTAGGAGATCCGAAGAAGACGAGCTAGGGTTGGCTCGGACTTACAGA 455  
 QY 413 CACCTGAGATGAGAGATTGGCTTATGATGACGCCGCTTAAATATGCTGAGCTAAG 472  
 Db 456 CGCCGAGAGCGCGGGTGGCGTACGACCGCGCGCTTCACTCAGAGGATGAAG 515  
 QY 473 CTAGGCTTAATTTCTCATTTGATTGTTGCAATATTTCCGAGCCCGTTAGATPAAC 532  
 Db 516 CTAGGCTGAATTTTCCGCAATTGATTGTTCTTGAATATGAGCCGGTTAGATTAGC 575

QY 533 CGAAGAAACGTTCCCTG 550  
 Db 576 CTCGCGCTCGCTCGCCG 593

**RESULT 6**  
**AVS52445** 563 bp mRNA linear EST 23-FEB-2004  
**LOCUS** AVS52445 Arabidopsis thaliana roots Columbia Arabidopsis thaliana  
**DEFINITION** CDNA clone R229h0R 5', mRNA sequence.  
**ACCESSION** AVS52445  
**VERSION** AVS52445.1 GI:8723858  
**KEYWORDS** EST.  
**SOURCE** Arabidopsis thaliana (thale cress)  
**ORGANISM** Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

**REFERENCE**  
 1 (bases 1 to 563)

**AUTHORS** Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
**TITLE** A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

**JOURNAL** DNA Res. 7 (3), 175-180 (2000)  
**MEDLINE** 20363093  
**PUBMED** 10907847

**COMMENT** Contact: Erika Asamizu  
 The First Laboratory for Plant Gene Research  
 Kazusa DNA Research Institute  
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
 Email: asamiz@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

**FEATURES**  
 source  
 location/Qualifiers  
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 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /ecoli\_type="Columbia"  
 /db\_xref="taxon:3702"  
 /db\_xref="R229h02R"  
 /issue\_type="roots"  
 /clone\_lib="Arabidopsis thaliana roots Columbia"  
 /note="Vector: pBluescriptII SK-, Site\_1: EcoRI; Site\_2: XhoI"

**ORIGIN**

Query Match 16.8%; Score 133; DB 1; Length 563;  
 Best Local Similarity 65.1%; Pred. No. 4.6e-24;  
 Matches 196; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 233 CGAAGCTGTCAAGAGATTCTGTGTGGAAACCCGCCAAGAGCGCGCCGAGAG 292  
 Db 260 CCGTACCTCTCCGGGAGGAAATPAACCTCCGCGACGAAGCGAGTGCACAG 319  
 QY 293 GTTGTTCGAAGATTGGAACCGGTATAGGGCGTTAGACGCGCGCGTGGGGAAGTTG 352  
 Db 320 CGCCGAGGCAAGAGGGAGTGCAGTACAGAGATGAGAGAGCGCCGTGGGGAATTG 379  
 QY 353 CGCGGAGATPAAGGATCCGAAAAAGAAAGATCCAGATTGTGGTACATACAGA 412  
 Db 380 CGCGGAGATTAGGATCCGAAGAAGACGAGCTAGGGTTGGCTCGGACTTACAGA 439  
 QY 413 CACCTGAGATGAGAGATTGGCTTATGATGACGCCGCTTAAATATGCTGAGCTAAG 472  
 Db 440 CGCCGAGAGCGCGGGTGGCGTACGACCGCGCGCTTCACTCAGAGGATGAAG 499  
 QY 473 CTAGGCTTAATTTCTCATTTGATTGTTGCAATATTTCCGAGCCCGTTAGATPAAC 532  
 Db 500 CTAGGCTGAATTTTCCGCAATTGATTGTTCTTGAATATGAGCCGGTTAGATTAGC 559

QY 533 C 533  
 Db 560 C 560

**RESULT 7**  
**BE449392** 591 bp mRNA linear EST 18-MAY-2001  
**LOCUS** BE449392 Arabidopsis thaliana roots Cornell University Lycopersicon  
**DEFINITION** EST356151 L. hirsutum trichome, Cornell University Lycopersicon  
**ACCESSION** BE449392  
**VERSION** BE449392.1 GI:9454895  
**KEYWORDS** EST.  
**SOURCE** Lycopersicon hirsutum (Solanum hirsutum)  
**ORGANISM** Lycopersicon hirsutum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

**REFERENCE**  
 1 (bases 1 to 591)  
 van der Hoeven, R.S., Bezzerides, J.L., Materin, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Niernan, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.  
 Generation of ESTs from wild tomato (Lycopersicon hirsutum)



JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: CUGI

FEATURES	Location/Qualifiers
source	1. .591

Query Match	16.8%	Score 13;	DB 2;	Length 591;
Best Local Similarity	65.9%	Pred. No. 4.6e-24;		
Matches 193; Conservative	0;	Mismatches 100;	Indels 0;	Gaps 0;

QY	278	CGGCGGCGCGAGAGAGTGTTCGAAGAGTTGGAACCGGTATTAAGGGCGTTTGA	CGGCGGCG
Db	295	CGGAGCTCCGGCGCGCTGAACAACCGAAGAGACATTATATGAGCGTTTGA <td>CGGCGT</td>	CGGCGT
QY	338	CGTGGGGGAAATTGCGCGCGGAGATTAAAGATCCGAAAAAGAAAGATCCAGATTTTGGT	397
Db	355	CGTGGGGGAAATTTGCGCGCGAGATTAGAGATCCGGCAAGAA	CGGACTAGGGTTGGC 414
QY	398	TGGGTACATACGAGACACTGAGATGAGAGATTGCTATGATCCACCGCGTTATA	457
Db	415	TGGAACTATGAAACAGCTGAAGAGCTGCAATTGCTTATGATTAACCTGCTATTAA	474
QY	458	TGCGTGGAGCTAAAGCTAAGCTTAATTTCTCATTTGATTGTTGCAATATTTCCGAGC	517
Db	475	TGAGAGATCAAAAGCACATTGGAATTTCCGCAACCGGATCGTTTGAATGACCAAGAC	534
QY	518	CCGTTAAGTAAACCCGAGAAAGCTTTCCTCGGAGCGCTTCTACGACGTGG	570
Db	535	CGGTTTCAGTTACGCGGAAAGGAGGAGCATGCGCGGAACCGGACAGCTGCTGG	587

RESULT 8	AV822925	LOCUS	DEFINITION
	AV822925	663 bp	mRNA
	AV822925	RAFL5	Arabidopsis thaliana cDNA clone RAFL05-13-E10 5', mRNA sequence.

REFERENCE  
AUTHORS  
1 (bases 1 to 663)  
Seki, M., Narusaka, M., Ishida, J., Kamuya, A., Satou, M., Nakajima, M.,  
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y.  
and Shinozaki, K.  
TITLE  
JOURNAL  
COMMENT  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a *Sac*I/XhoI insert. please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

FEATURES	Location/Qualifiers
source	1. .663

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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL05-13-E10"
/dev_stage="rosette plants"
/lab_no="SOLR"
/clone_id="RAFL5"
/note="Site_1: Sact; Site_2: XhoI; subjected to
dehydration-treated(1,2,5,10,24 hr)"

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Qy	533	C	533
	591	C	591
Db			

RESULT 9	490 bp	mRNA	linear	EST 15-NOV-2002
CA520877				
LOCUS	CA520877			
DEFINITION	KS110108B10 KS11 Capsicum annuum cDNA, mRNA sequence.			

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (pages 1 to 490)  
Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Paik, H.-S.,  
Hur, C.-G. and Choi, D.  
Generation of Expressed Sequence Tags from Hot Pepper (*Capiscum  
annuum* L.) and Sequence Analysis in Relation to Hypersensitive  
Response Against Pathogen  
Unpublished. (2001)  
Contact: Doll Choi  
Genome Research Center and National Center for Genome Information  
Korea Research Institute of Bioscience and Biotechnology  
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea

Tel: 82-42-860-4340  
 Fax: 82-42-860-4309  
 Email: doi@mail.krdb.re.kr  
 Plate: 018 row: B column: 10.

## FEATURES

Location/Qualifiers

1. 490

/organism="Capsicum annuum"

/mol\_type="mRNA"

/db\_xref="taxon:4072"

/clone\_lib="KS11"

## ORIGIN

Query Match 16.8%; Score 132.8; DB 6; Length 490;  
 Best Local Similarity 67.1%; Pred. No. 5.1e-24;  
 Matches 188; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 305 ATTGGAACCGGTATTAGGCGCTTAAAGCGCGCGCTTGGGGGAAAGTTCCGGCGGAGATTA 364  
 DB 179 ATAGGAGAGATACATAGAGGGGTGAGCGGAGCAATGGGGTACGTTTCTGAGAGATTA 238  
 QY 365 GGGATCCGAAAAAGAAAGATCCAGATTGGTGGGTACATACGAGACACCTGAGATG 424  
 DB 239 GAGATCCGAAATAGAGAGCGCGAGGCTATGGCTAGAACTTATGAGACTCTTGAGGATG 298  
 QY 425 CAGCATTTGGCTTATGATGACCGCGCTTAAATATGCGTGAAGCTAAAGCTTAATT 484  
 DB 299 CAGCATTTGGCTTATGACCAAGCGCATTCAAAATTGCTGCGAAGCTCGGCTCAATT 358  
 QY 485 TTCCCTCATTTGATTGTTTGAATATTTCCGAGCCGTTAGATTAACCGAGAAAAGTT 544  
 DB 359 TTCTTAGTTGATGAGCTCGGAGCGATGCGTAAGCTGATAGACTAACCGTGAAGCGCCGTA 418  
 QY 545 TCCCTGCGAGCGCTTACAGAGCTGCTGCTTCTTCTTC 584  
 DB 419 CGGATCGCCCGAGCATGACTTCTCTCTGATCATC 458

## RESULT 10

CB078370

LOCUS

DEFINITION h66g10.g1 Hedycotis terminalis flower - Stage 2 (NYBG) Hedycotis

terminalis cDNA clone h66g10, mRNA sequence.

ACCESSION

CB078370.1 GI:27891807

VERSION

KEYWORDS

SOURCE

ORGANISM

Hedycotis terminalis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiales; Gentianales; Rubiaceae; Rubioidae;

Spermacoceae; Hedycotis.

1 (bases 1 to 636)

Leveque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhi,N.N.,

O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,

Benley,P. and Stevenson,D.

Expressed tag sequences from Hedycotis terminalis flower - Stage 2

(NYBG)

Unpublished (2003)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mccombie@cshl.org

Plate: h66 row: 9 Column: 10

Seq primer: -21M13UnivRev

High quality sequence stop: 636.

Location/Qualifiers

1. 636

/organism="Hedycotis terminalis"

/mol\_type="mRNA"

/db\_xref="taxon:219667"

## ORIGIN

Query Match 16.7%; Score 132.6; DB 6; Length 636;  
 Best Local Similarity 69.5%; Pred. No. 6e-24;  
 Matches 180; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 245 AGGAGATTCTGTTGGGAAACCCCGCCAGAAAGCGCGCGGAGGAGTGTTCGAAGG 304  
 DB 281 AGGAGTACAGCAAGATTGTCCGCGCGCGCGCGAGTGGAAAGCACTGATACCG 340  
 QY 305 ATTGAACCGGTATTAAGCGCGTTAGACGCGCGCGTGGGGAAGTTCCGCGCGAGATTA 364  
 DB 341 AGTGAAGCGCATACAAAGTGTTCGAGAGAGCGCGTGGGGAAGTTCCGCGCGAGATTA 400  
 QY 365 GGGATCCGAAAAAGAAAGATCCAGATTGTTGGGTACATACGACACCTGAGATG 424  
 DB 401 GAAACCCGGGGAAGAAAGATCAGAAATATGCTGGGAAAGTACGAGACGCGGAGATG 460  
 QY 425 CAGCATTTGGCTTATGATGACCGCGCTTAAATATGCGTGAAGCTAAAGCTTAATT 484  
 DB 461 CCGATTGGCTTACGACCGCGCGCTTACCACTGAGGGGTGCAAGCTTAAGCTTAATT 520  
 QY 485 TTCCCTCATTTGATTGTTTC 503  
 DB 521 TTCCACATATGATTGATC 539

## RESULT 11

BF275652

LOCUS

DEFINITION GA\_Eb0024J23f Gossypium arboreum 7-10 dpa fiber library Gossypium

arboreum cDNA clone GA\_Eb0024J23f, mRNA sequence.

ACCESSION

BF275652.1 GI:11206722

VERSION

KEYWORDS

SOURCE

ORGANISM

Gossypium arboreum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

1 (bases 1 to 903)

Wing,R.A., Fritch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,

Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.

An integrated analysis of the genetics, development, and evolution

of the cotton fiber

Unpublished (2000)

Contact: Wing RA

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: twing@clemson.edu

Seq primer: TAATGACACTCACTAAGG

High quality sequence start: 48

High quality sequence stop: 683.

Location/Qualifiers

1. 903

/organism="Gossypium arboreum"

/mol\_type="mRNA"

/strain="AKA"

/cultivar="8400"

/db\_xref="taxon:29729"

/clone="GA\_Eb0024J23f"



Db 10 TATAGAGGCGTATAGACAGCGTCCTGGGGGAAATTTGCGCGAGATTTAGATCCGGCG 69  
 QY 376 AAGAAAGATCCGAGATTTGTTGGGTACATACGAGACCTGAGGATGACAGATTGGCT 435  
 Db 70 AAGAACGAGACTGAGGTTGGCTTGGAGCTGACGAAACGCTGAAAGAGAGCTGCAATTTGCT 129  
 QY 436 TATGATGACAGCCGCTTTAATATGCGTGAGCTAAAGCTTAAATTTTCTCATTTG 495  
 Db 130 TATGATTAAGCTGCTTATGAAATGAGAGATCAAAAGCATTGTAATTTCCGACCGG 189  
 QY 496 ATTGTTTCAATTTTCCGAGCCCTTAAAGTAAACCGAGAAAAGTTTCCCTCGGAG 555  
 Db 190 ATCGGTTTGAATTAACCGAGACCGGTTGAGATTACGCGAAAGGCGAGCATGCGCGAA 249  
 QY 556 CCTTTACGACGCTCG 570  
 Db 250 CCGGCAAGCTCGTCG 264

RESULT 14  
 AM034216 575 bp mRNA linear EST 18-MAY-2001  
 LOCUS EST277787 tomato callus, TAMU Lycopersicon esculentum cDNA clone  
 DEFINITION CLEC32P18 similar to Pti4, mRNA sequence.  
 ACCESSION AM034216  
 VERSION AM034216.1 GI:5892972  
 KEYWORDS EST.  
 SOURCE Lycopersicon esculentum (tomato)  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  
 1 (bases 1 to 575)  
 AUTHORS Alcalá, J., Vrebalov, J., White, R., Matern, A.L., Vision, T.,  
 Holt, I.E., Liang, F., Upcon, J., Craven, M.B., Bowman, C.L., Alm, S.,  
 Romling, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and  
 Giovannoni, J.  
 REFERENCE Generation of ESTs from tomato callus tissue  
 Unpublished (1999)  
 JOURNAL Contact: CUGI  
 COMMENT Clemson University Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.

FEATURES  
 Source Location/Qualifiers  
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 /organism="Lycopersicon esculentum"  
 /mol\_type="mRNA"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="CLEC32P18"  
 /tissue\_type="callus"  
 /dev\_stage="25-40 days old"  
 /lab\_host="Xl1-Blue MRF"  
 /clone\_lib="tomato callus, TAMU"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
 XhoI; supplier: Giovannoni laboratory; CLEC - Cotyledons  
 of seedlings 7-10 days post-germination were excised, cut  
 at both ends and placed on MS medium with no selection.  
 Mixed callus was harvested at 25 and 40 days and included  
 undifferentiated masses. Tomato Callus EST library"

## ORIGIN

Query Match 16.2%; Score 128.2; DB 2; Length 575;  
 Best Local Similarity 64.8%; Pred. No. 8.6e-23;  
 Matches 190; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 278 CCGCGGCGGAGAGAGTTGTTCGAAGATTGACCGGCTTAAACGCGCG 337  
 Db 278 CCGGACCTCCGCGGCTGAAACCGGAAAGAGACATTATGAGCCGTTAGACGCGTC 337

QY 338 CGTGGGGGAATTCCTCGCGCGAGATTAAGGATCCGAAAAAGAAAGATCCAGATTGGT 397  
 Db 338 CGTGGGGGAATTCCTCGCGCGAGATTAAGATCCGCGAAAGACGAGCTAGGGTTGGC 397  
 QY 398 TGGGTATATCGAGACACCGAGATGACGATTTGGCTTATGATGAGCGCGTTAAAT 457  
 Db 398 TTGGAACGTACGAAACGCTGAAAGAGCTGCAATTCCTTATGATTAAGCTGCTTATGAA 457  
 QY 458 TGGCGAGCTAAAGCTTAAATTTTCTCATTTGATTTGATGCAATATTTCCGAGC 517  
 Db 458 TGAGAGATCAAAAGCAGCATTTGATTTCCCGACCGGATTCGTTGATGAAACGCGAAC 517  
 QY 518 CCGTTAGATTAACCGGAGAAACGTTTCCCTCGGAGGCTTTCACGACTG 570  
 Db 518 CCGTTGAGATTACGCGGAAAGCGAGCATCCGCGAACCAGCAACTGCTG 570

RESULT 15  
 AM584731 638 bp mRNA linear EST 07-SEP-2000  
 LOCUS N210846e MHAM Medicago truncatula/Gloms versiforme mixed EST  
 DEFINITION library cDNA clone MHAM-7M11, mRNA sequence.  
 ACCESSION AM584731 GI:7261785  
 VERSION AM584731.1  
 KEYWORDS EST.  
 SOURCE Medicago truncatula/Gloms versiforme mixed EST library  
 ORGANISM Medicago truncatula/Gloms versiforme  
 Eukaryota; mixed EST libraries.  
 1 (bases 1 to 638)  
 REFERENCE Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D.,  
 Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.  
 ESTs from roots of Medicago truncatula after colonization with  
 Gloms versiforme  
 Unpublished (2000)  
 JOURNAL Contact: Harrison M.J.  
 COMMENT Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73401  
 Tel: 580-223-5810  
 Fax: 580-221-7380  
 Email: [mj.harrison@noble.org](mailto:mj.harrison@noble.org)  
 Other name: MHAM-7a-G06; Date: 3/14/00; Updated to the Database of  
 Expressed Sequence Tags (dbEST) on 04/27/00; More information is  
 available at '<http://chryslie.tamu.edu/medicago>'.  
 Seq primer: T3.

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 Source Location/Qualifiers  
 1..638  
 /organism="Medicago truncatula/Gloms versiforme mixed EST  
 library"  
 /mol\_type="mRNA"  
 /cultivar="Medicago truncatula genotype A17"  
 /db\_xref="taxon:119092"  
 /clone="MHAM-7M11"  
 /tissue\_type="roots colonized with Gloms versiforme"  
 /dev\_stage="Roots harvested at 10, 17, 22, 31 and 38 days  
 post-inoculation with Gloms versiforme. The library was  
 made from a mixture of RNA from each of these stages."  
 /lab\_host="E. coli strain XL0LR"  
 /clone\_lib="MHAM"  
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
 XhoI; cDNA was prepared from polyA+ enriched RNA from  
 roots harvested at 10, 17, 22, 31 and 38 days  
 post-inoculation with Gloms versiforme. The cDNA was  
 directionally ligated into the Uniap XR vector from  
 Stratagene and packaged using Gigapack III Gold packaging  
 extracts. Plasmids containing cDNA inserts were excised  
 from the recombinant lambda-Zap phage using Ex-aseIst  
 helper phage and propagated in XL0LR cells."

## ORIGIN

Query Match 16.2%; Score 128; DB 2; Length 638;  
 Best Local Similarity 73.2%; Pred. No. 9.9e-23;  
 Matches 164; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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QY 307 TGAACCGTATAGGCGTTAGACGGCGCCGTGGGGAAAGTTCCGCGCGAGATAAG 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 236 TGAAGCGGTACAAAGGCGTGAAGCCATGGGGAAAGTTCCGCGCAGAGATAAGA 295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 367 GATCCGAAAAAAGAGATCCAGGATTGGTTGGGTACATACGAGACACTGAGGATGCA 426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 296 GATCCAAAAAAGAGATGGTGTAGGATTGGCTTGTACTTATGTGACTGAGGAGAAACA 355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 427 GCATTGGCTATGATGACGCGCGTTTAAATATGCGTGAAGCTAAGCTTAATTTT 486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 356 GCTTGGCTTACGCAAGGCTGCTTTAAGATGCGTGGCCGAAAGGCCAAGCTTAATTTT 415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 487 CCTCATTGATGGTTGGAATATTTCCGACCCGTTAGATPAA 530
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 416 CCCCACTCAITGGCTGTGATGTGTTACACGAGGCCAGAGAA 459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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 Job time : 3392 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2005, 22:06:55 ; Search time 165 Seconds  
(without alignments)  
475.832 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 203  
Sequence: 1 MEEETISVSDRFLSLIEEH.....SSSSSSSSSENSGCKRRY 203

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: \_geneseqp1980s:\*\n2: \_geneseqp1990s:\*\n3: \_geneseqp2000s:\*\n4: \_geneseqp2001s:\*\n5: \_geneseqp2002s:\*\n6: \_geneseqp2003as:\*\n7: \_geneseqp2003bs:\*\n8: \_geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	203	100.0	203	3	AAy97228
2	19	9.4	183	3	AAy97228
3	19	9.4	183	3	AAy97228
4	19	9.4	183	3	AAy97228
5	19	9.4	183	3	AAy97228
6	19	9.4	183	3	AAy97228
7	19	9.4	183	3	AAy97228
8	19	9.4	183	3	AAy97228
9	19	9.4	183	3	AAy97228
10	19	9.4	183	3	AAy97228
11	19	9.4	183	3	AAy97228
12	19	9.4	183	3	AAy97228
13	19	9.4	183	3	AAy97228
14	19	9.4	183	3	AAy97228
15	19	9.4	183	3	AAy97228
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18	19	9.4	183	3	AAy97228
19	19	9.4	183	3	AAy97228
20	19	9.4	183	3	AAy97228
21	19	9.4	183	3	AAy97228
22	19	9.4	183	3	AAy97228
23	19	9.4	183	3	AAy97228
24	19	9.4	183	3	AAy97228
25	19	9.4	183	3	AAy97228

26	17	8.4	139	8	AD061811	Ad061811 Transcrip
27	17	8.4	139	8	AD062997	Ad062997 Transcrip
28	17	8.4	201	4	AAE02540	AAE02540 A. thalia
29	17	8.4	201	4	AD030756	Ad030756 Plant yie
30	17	8.4	201	8	AD143767	Ad143767 Plant tra
31	17	8.4	201	8	AD001637	Ad001637 Thalecres
32	17	8.4	201	8	AD003313	Ad003313 Thalecres
33	17	8.4	201	8	AD062889	Ad062889 Transcrip
34	17	8.4	207	4	AAE02554	AAE02554 A. thalia
35	17	8.4	207	4	AD055696	Ad055696 Thalecres
36	17	8.4	207	8	AD001641	Ad001641 Transcrip
37	17	8.4	207	8	AD061543	Ad061543 Transcrip
38	17	8.4	282	8	AD142040	Ad142040 Plant tra
39	17	8.4	282	8	AD142694	Ad142694 Plant tra
40	17	8.4	282	8	AD002947	Ad002947 Thalecres
41	16	7.9	131	8	AD143273	Ad143273 Plant tra
42	16	7.9	131	8	AD063660	Ad063660 Transcrip
43	16	7.9	173	3	AAE09634	AAE09634 Arabidops
44	16	7.9	173	3	AAE09952	AAE09952 Arabidops
45	16	7.9	218	3	AAE09951	AAE09951 Arabidops

#### ALIGNMENTS

RESULT 1  
ID AAY97228 standard; protein; 203 AA.  
XX AAY97228;

XX AAY97228;

XX 19-DEC-2000 (first entry)

XX Plant transcription factor AP2 DNA-binding domain polypeptide.

XX AP2: transcription factor; plant metabolism; metabolite; primary;

XX secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;

XX food colouring; flavouring; fragrance; antimicrobial; pathogenic;

XX insecticide; gene expression; modulation.

XX Catharanthus roseus.

XX W0200046383-A2.

XX 10-AUG-2000.

XX 07-FEB-2000; 2000MO-NL000075.

XX 05-FEB-1999; 99DK-00000158.

XX 10-FEB-1999; 99US-0119388P.

XX (UYLE-) RIKSUNIV LEIDEN.

XX Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW;

XX WPI; 2000-499380/44.

XX N-PSDB; AAA53745.

XX Modulating level of metabolites and stress resistance in recombinant

XX cells for synthesis of plant metabolites such as alkaloids including

XX terpenoid indole alkaloids, by providing transcription factor to the

XX cell.

XX Disclosure; Page 97-98; 101pp; English.

XX Many plant secondary metabolites have value as pharmaceuticals, food

XX colourings, flavours and fragrances. Some plant secondary metabolites are

XX linked to plant or plant cell defence mechanisms and may confer to the

XX plant antimicrobial activity, protection against UV light, herbivores,

XX pathogens, insects and nematodes. Plant secondary metabolites such as

XX terpenoid indole alkaloids (TIA) represent a class of pharmaceutically

XX useful compounds which naturally occur in many plant species. New methods

XX are described which modulate the expression of one or more genes involved

CC in the biosynthesis of plant metabolites or their precursors in plant  
CC cells. The method comprises inserting into a plant cell a sequence  
CC encoding a transcription factor comprising an AP2 DNA-binding domain and  
CC by modifying the expression of that transcription factor. Transcription  
CC factors comprising an AP2 DNA-binding domain are useful as central  
CC regulators of complex metabolite pathways involving numerous target genes  
CC for such transcription factors. This means that the yield of commercially  
CC valuable metabolite compounds can be enhanced and the tolerance of plants  
CC towards exogenous stress factors can be influenced. The method is useful  
CC for modulating the level of one or more metabolites. By providing a  
CC transcription factor to the cell the level of the metabolite is enhanced  
CC by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to  
CC a cell to which the transcription factor is not provided  
CC  
XX  
SQ Sequence 203 AA;

Query Match 100.0%; Score 203; DB 3; Length 203;  
Best Local Similarity 100.0%; Pred. No. 1,5e-181;  
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSEETISVSDRFLSLIEEHLISDNDSSSEITSTEENWBERIFADFLNMGSEIQRGS 60  
Db 1 MSEETISVSDRFLSLIEEHLISDNDSSSEITSTEENWBERIFADFLNMGSEIQRGS 60  
QY 61 PSSESCQSNMMAESCQEDSVGTTPPAAGCGCKDMNRYKVRRRPWCXFAEIRDPK 120  
Db 61 PSSESCQSNMMAESCQEDSVGTTPPAAGCGCKDMNRYKVRRRPWCXFAEIRDPK 120  
QY 121 KSRILWLTGTEPEDAALAYDAAEFMGRGAKARLNPPLIGSNISGPVVRNKKPPEP 180  
Db 121 KSRILWLTGTEPEDAALAYDAAEFMGRGAKARLNPPLIGSNISGPVVRNKKPPEP 180  
QY 181 STTSSSSSSSSSSSGRKKRRY 203  
Db 181 STTSSSSSSSSSSSGRKKRRY 203

RESULT 2  
AAC24801  
ID AAC24801 standard; protein; 183 AA.

XX AAC24801;  
AC  
XX  
DT 17-OCT-2000 (first entry)  
XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 28613.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX  
PD 06-SEP-2000.

XX  
PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
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PR 07-MAY-1999; 99US-0132683P.  
PR 11-MAY-1999; 99US-0134256P.  
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PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135134P.  
PR 21-MAY-1999; 99US-0135233P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
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PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140655P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
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PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
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PR 19-JUL-1999; 99US-0144332P.  
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PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.



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PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145122P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
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PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
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PR 11-AUG-1999; 99US-0148319P.
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Query Match 9.4%; Score 19; DB 3; Length 183;
Best Local Similarity 100.0%; Pred. No. 2,5e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 51 GVRRRPWGKFAAIRDPKK 69

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XX AC AAAG34782;
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DT 18-OCT-2000 (first entry)
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XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
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XX OS Arabidopsis thaliana.
XX
XX PN EP1033405-A2.
XX
XX PD 06-SEP-2000.
XX
XX PF 25-FEB-2000; 2000EP-00301439.
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Query Match 9.4%; Score 19; DB 3; Length 183;  
Best Local Similarity 100.0%; Pred. No. 2.5e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRPVGKFAAETIRDPKK 120  
Db 51 GVRRPVGKFAAETIRDPKK 69

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ID ADM72373 standard; protein; 202 AA.  
AC ADM72373;  
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XX  
DT 01-JUL-2004 (first entry)  
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XX  
DE Soybean NRTF1c polypeptide.

XX Plant; nematode-regulated polypeptide; calcium dependent protein kinase;  
XX CDPK; nematode-responsive transcription factor 1; NRTF1;  
XX nematode-responsive protein; NRP; caffeic acid 7-O-methyltransferase;  
XX 7OM; inositol 5-phosphatase; IPP; nematocidal; gene therapy;  
XX nematode resistance; soybean; enzyme; NRTF1c.

XX Glycine max.  
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XX PN WO2004029222-A2.  
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XX PD 08-APR-2004.  
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XX PF 30-SEP-2003; 2003WO-US031029.  
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XX PR 30-SEP-2002; 2002US-0414771P.

XX (PION-) PIONEER HI-BRED INT INC.  
XX  
XX Hu X, Lu G;  
XX  
XX WPI: 2004-316104/29.  
XX  
XX N-PSDB; ADM72372.

XX New isolated nucleic acid molecules encoding nematode-responsive  
XX proteins, useful for conferring or improving nematode resistance in  
XX plants.

XX  
XX PS Claim 26; SEQ ID NO 11; 143pp; English.

XX The invention relates to pathogen-responsive genes that encode a nematode  
XX -regulated polypeptides. The proteins of the invention include calcium  
XX dependent protein kinase (CDPK), nematode-responsive transcription factor  
XX 1 (NRTF1), nematode-responsive protein (NRP), caffeic acid 7-O-  
XX methyltransferase (7OM) or inositol 5-phosphatase (IPP) polypeptides. The  
XX nucleic acid molecule encoding the polypeptides are operably linked to a  
XX promoter that drives expression in a host cell. The composition and  
XX methods are useful for conferring or improving nematode resistance in  
XX plants. The present sequence represents a soybean NRTF1c polypeptide.

XX  
XX SO Sequence 202 AA;

Query Match 9.4%; Score 19; DB 8; Length 202;  
Best Local Similarity 100.0%; Pred. No. 2.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRPVGKFAAETIRDPKK 120  
Db 79 GVRRPVGKFAAETIRDPKK 97

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AC ADM72375;  
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XX  
DT 01-JUL-2004 (first entry)  
XX  
XX

XX  
XX DE Soybean NRTF1d polypeptide.

XX Plant; nematode-regulated polypeptide; calcium dependent protein kinase;  
XX CDPK; nematode-responsive transcription factor 1; NRTF1;  
XX nematode-responsive protein; NRP; caffeic acid 7-O-methyltransferase;  
XX 7OM; inositol 5-phosphatase; IPP; nematocidal; gene therapy;  
XX nematode resistance; soybean; enzyme; NRTF1d.

XX Glycine max.  
XX  
XX OS  
XX  
XX PN WO2004029222-A2.  
XX  
XX PD 08-APR-2004.

XX  
XX PF 30-SEP-2003; 2003WO-US031029.  
XX  
XX PR 30-SEP-2002; 2002US-0414771P.

XX (PION-) PIONEER HI-BRED INT INC.

XX  
XX Hu X, Lu G;  
XX  
XX WPI: 2004-316104/29.  
XX  
XX DR N-PSDB; ADM72374.

XX  
XX PT New isolated nucleic acid molecules encoding nematode-responsive  
XX proteins, useful for conferring or improving nematode resistance in  
XX plants.

XX PS Claim 26; SEQ ID NO 13; 143pp; English.

XX The invention relates to pathogen-responsive genes that encode a nematode  
XX -regulated polypeptides. The proteins of the invention include calcium  
XX dependent protein kinase (CDPK), nematode-responsive transcription factor  
XX 1 (NRTF1), nematode-responsive protein (NRP), caffeic acid 7-O-  
XX methyltransferase (7OM) or inositol 5-phosphatase (IPP) polypeptides. The  
XX nucleic acid molecule encoding the polypeptides are operably linked to a  
XX promoter that drives expression in a host cell. The composition and  
XX methods are useful for conferring or improving nematode resistance in  
XX plants. The present sequence represents a soybean NRTF1d polypeptide.

XX  
XX SO Sequence 202 AA;

Query Match 9.4%; Score 19; DB 8; Length 202;  
Best Local Similarity 100.0%; Pred. No. 2.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRPVGKFAAETIRDPKK 120  
Db 79 GVRRPVGKFAAETIRDPKK 97

RESULT 6  
AAG24800  
ID AAG24800 standard; protein; 212 AA.

XX AAG24800;  
AC  
XX 17-OCT-2000 (first entry)  
DT  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 28612.  
DE  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KM hybridization assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS  
XX EP1033405-A2.  
PN  
XX 06-SEP-2000.  
PD  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
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XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
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PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
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DT 18-OCT-2000 (first entry)

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KM termination sequence.

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PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161933P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 9.4%; Score 19; DB 3; Length 226;  
Best Local Similarity 100.0%; Pred. No. 3e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GVRRRPMGKFAAIRDPKX 120  
Db 94 GVRRRPMGKFAAIRDPKX 112

RESULT 9

AAG24799

ID AAG24799 standard; protein; 226 AA.

XX AAG24799;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 28611.

KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132837P.  
PR 11-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135133P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 17-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139452P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140655P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.



PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148568P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-015138P.  
PR 01-SEP-1999; 99US-015130P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-015569P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.

PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-016193P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 9.4%; Score 19; DB 3; Length 226;  
Best Local Similarity 100.0%; Pred. No. 3e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAEIRDPKK 120  
Db 94 GVRRRPWGKFAEIRDPKK 112

RESULT 10  
ID AAE02464 standard; protein; 226 AA.  
AC AAE02464;  
XX 10-AUG-2001 (first entry)  
XX DE Arabidopsis thaliana transcription factor G22.  
XX KM Transcription factor; environmental stress tolerance; gene therapy;  
XX KW plant structure; plant development.  
XX OS Arabidopsis thaliana.  
XX FH Key Location/Qualifiers  
FT Domain 89..157 /note="Conserved domain"  
XX FT  
XX FN WO200136598-A1.  
XX PD  
XX 25-MAY-2001.  
XX PF 14-NOV-2000; 2000MO-US031458.  
XX PR 17-NOV-1999; 99US-0166228P.  
XX PR 17-APR-2000; 2000US-0197899P.  
XX PR 22-AUG-2000; 2000US-0227439P.  
XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
XX PA (PINE/) PINEDA O.

PA (YUGG/) YU G.  
 PA (CREE/) CREELMAN R.  
 PA (RIEC/) RIECHMANN J. L.  
 PA (HEAR/) HEARD J.  
 PA (RATC/) RATCLIFFE O.  
 PA (REUB/) REUBER L.  
 PA (KEDD/) KEDDIE J.  
 XX  
 PI Pineda O, Yu G, Creelman R, Riechmann JL, Heard J, Ratcliffe O,  
 PI Reuber L, Keddie J;  
 XX  
 DR WPI: 2001-336000/35.  
 DR N-PSDB; AAD06444.  
 XX  
 PT Nucleic acids encoding plant transcription factor polypeptides, useful  
 PT for altering the environmental stress tolerance characteristics of  
 PT plants.  
 XX  
 PS Claim 4; Page 55-56; 116pp; English.  
 XX  
 CC The present amino acid sequence is Arabidopsis thaliana transcription  
 CC factor. This novel transcription factor is useful for modifying a plant's  
 CC phenotype in desirable ways, such as modifying a plants environmental  
 CC stress. The transcription factor is encoded by environmental stress  
 CC tolerance gene derived from Arabidopsis thaliana. The transcription  
 CC factors and the genes encoding them are used to alter the structure and  
 CC developmental characteristics of plants such as soybean, wheat, corn,  
 CC potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf,  
 CC banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot,  
 CC cauliflower, coffee, onion, cucumber, eggplant, grapes, honey dew,  
 CC lettuce, mango, melon, papaya, peas, pepper, pineapple, spinach, squash,  
 CC sweet corn, tobacco, tomato, watermelon, roseaceous fruits and/or  
 CC vegetable brassicas. These sequences are also used for modifying traits  
 CC associated with environmental stress tolerance, such as freezing,  
 CC chilling, heat, drought, water saturation, salt, photoconditons,  
 CC radiation and ozone. The transcription factors are used in gene therapy  
 CC  
 SQ Sequence 226 AA;  
 Query Match 9.4%; Score 19; DB 4; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 3e-09;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 102 GVRRRPWGKFAAEIRDPKK 120  
 Db 94 GVRRRPWGKFAAEIRDPKK 112  
 RESULT 11  
 ADE37189  
 ID ADE37189 standard; protein; 226 AA.  
 XX  
 AC ADE37189;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Plant yield related protein from clone G22.  
 XX  
 KW transcription factor; tolerance; environmental condition;  
 KW microbial disease; fungal disease; viral disease; pest infestation;  
 KW herbicide sensitivity; heavy metal tolerance; heavy metal uptake;  
 KW growth improvement; photocondition; nutrient uptake; hormone sensitivity;  
 KW transgenic plant.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN WO2003014327-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 09-AUG-2002; 2002WO-US026966.  
 XX  
 PR 09-AUG-2001; 2001US-0310847P.

PR 19-NOV-2001; 2001US-0336049P.  
 PR 11-DEC-2001; 2001US-0338692P.  
 PR 14-JUN-2002; 2002US-00171468.  
 XX  
 PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.  
 XX  
 PI Reuber TL, Riechmann JL, Heard JE, Jiang C, Adam LJ, Dubell AN,  
 PI Ratcliffe O, Pineda O, Yu GL, Broun PE;  
 XX  
 DR WPI: 2003-256576/25.  
 DR N-PSDB; ADE37188.  
 XX  
 PT New stress-related transcription factor polynucleotides and polypeptides,  
 PT useful for producing transgenic plants with e.g. improved tolerance to  
 PT diseases or pests, decreased herbicide sensitivity, or improved nutrient  
 PT uptake.  
 XX  
 PS Disclosure, SEQ ID NO 128; 470pp; English.  
 XX  
 CC The invention relates to a number of cDNA sequence and their encoded  
 CC proteins which are especially transcription factor cDNAs and their  
 CC proteins. The isolated or recombinant polynucleotide is useful for  
 CC producing a modified plant with a modified trait, e.g. enhanced tolerance  
 CC to environmental conditions, improved tolerance to microbial, fungal or  
 CC viral diseases, improved tolerance to pest infestation, decreased  
 CC herbicide sensitivity, improved tolerance of heavy metals, or enhanced  
 CC ability to take up heavy metals, improved growth under poor  
 CC photoconditons, improved nutrient uptake, or reduced hormone  
 CC sensitivity. The transgenic plants are useful for growing a progeny plant  
 CC comprising the desired trait. The polynucleotides and polypeptides are  
 CC also useful in bioinformatic search methods. This sequence represents one  
 CC of the proteins of the invention.  
 XX  
 SQ Sequence 226 AA;  
 Query Match 9.4%; Score 19; DB 7; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 3e-09;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 102 GVRRRPWGKFAAEIRDPKK 120  
 Db 94 GVRRRPWGKFAAEIRDPKK 112  
 RESULT 12  
 ADI41543  
 ID ADI41543 standard; protein; 226 AA.  
 XX  
 AC ADI41543;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Plant transcription factor #3.  
 XX  
 KW transgenic; plant; enhanced tolerance to abiotic stress;  
 KW glycosphate tolerance; hormone sensitivity; disease resistance;  
 KW sugar sensing; flowering; flower structure; stem bifurcation;  
 KW branching pattern; apical dominance; trichome; stem morphology;  
 KW root growth; root hair; seed development; cell proliferation;  
 KW cell differentiation; premature senescence; necrosis; plant size;  
 KW leaf morphology; seed morphology; seed biochemistry; root anihocyanin;  
 KW plant anihocyanin; light response; shade avoidance; bioinformatic;  
 KW transcription factor.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN US2004015927-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 25-FEB-2003; 2003US-00374780.  
 XX  
 PR 18-APR-2001; 2001US-00837944.

XX (SHER/) SHERMAN B K.  
 PA (RIEC/) RIECHMANN J L.  
 PA (JIANG/) JIANG C.  
 PA (HEAR/) HEARD J E.  
 PA (HAAR/) HAARE V.  
 PA (CREE/) CREELMAN R A.  
 PA (RATC/) RATCLIFFE O.  
 PA (ADAM/) ADAM L J.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J.  
 PA (BROU/) BROUN P E.  
 PA (PIILG/) PILGRIM M L.  
 PA (DUBE/) DUBELL A N.  
 PA (PINE/) PINEDA O.  
 PA (YUGG/) YU G.  
 XX Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V,  
 PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE,  
 PI Pilgrim ML, Dubell AN, Pineda O, Yu G,  
 XX WPI, 2004-132245/13.  
 DR N-PSDB; ADI41542.  
 PT New transgenic plant comprising a recombinant polynucleotide of any one  
 PT of more than 500 nucleotide sequences, useful in bioinformatic search  
 PT methods.  
 XX Claim 1; SEQ ID NO 6; 435bp; English.  
 XX The invention describes a transgenic plant comprising a recombinant  
 CC polynucleotide of any one of more than 500 nucleotide sequences fully  
 CC defined in the specification or its complement. The method of the  
 CC invention can be used to produce a plant having altered traits such as:  
 CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone  
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;  
 CC altered flower structure; change in stem bifurcations; altered branching  
 CC pattern; reduced apical dominance; reduced trichome density; lack of  
 CC trichomes; increased ectopic trichome development; altered trichome  
 CC development; increase in trichome number; altered stem morphology;  
 CC increased root growth; increased root hairs; altered seed development;  
 CC altered cell proliferation or cell differentiation; rapid development;  
 CC premature senescence; increased necrosis; increase in seedling or plant  
 CC size; decreased plant size; leaf morphology; seed morphology; seed  
 CC biochemistry; increase in root anthocyanins; increase in plant  
 CC anthocyanins; or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This is the amino acid sequence of a plant  
 CC transcription factor that can be used in the creation of a transgenic  
 CC plant with altered traits.  
 XX  
 XX Sequence 226 AA;  
 SQ  
 Query Match 9.4%; Score 19; DB 8; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 3e-09; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0;  
 QY 102 GVRRRPWGKFAAEIRDPK 120  
 Db 94 GVRRRPWGKFAAEIRDPK 112  
 RESULT 13  
 ADO01615  
 ID ADO01615 standard; protein; 226 AA.  
 AC ADO01615;  
 XX  
 DT 01-UTU-2004 (first entry)  
 XX  
 CC Thalecress transcription factor protein #14.  
 DE Thalecress transcription factor; plant; transgenic; abiotic stress;  
 XX  
 KM cold tolerance; heat tolerance; drought; osmotic stress;  
 KM phosphate limitation; potassium limitation; nitrogen limitation;  
 KM hormone sensitivity; disease resistance; sugar sensing; seed germination;  
 KM flowering; inflorescence architectural change;  
 KM meristem cell differentiation; phylloclaxy; apical dominance;  
 KM trichome development; seed development; premature senescence;  
 KM delayed senescence; lethality; necrosis; plant size; leaf morphology;  
 KM seed morphology; secondary metabolism; light response; shade avoidance.  
 XX Arabidopsis thaliana.  
 OS  
 XX  
 PN US2004045049-A1.  
 XX  
 PD 04-MAR-2004.  
 XX  
 XX 10-APR-2003; 2003US-00412699.  
 XX  
 XX 13-SEP-1999; 99US-00394519.  
 PR 21-JAN-2000; 2000US-00489376.  
 PR 17-FEB-2000; 2000US-00506720.  
 PR 22-MAR-2000; 2000US-00532591.  
 PR 22-MAR-2000; 2000US-00533029.  
 PR 22-MAR-2000; 2000US-00533030.  
 PR 22-MAR-2000; 2000US-00533392.  
 PR 22-MAR-2000; 2000US-00533648.  
 PR 06-APR-2000; 2000MO-US009448.  
 PR 16-NOV-2000; 2000US-00713994.  
 PR 27-MAR-2001; 2001US-00819142.  
 PR 17-APR-2001; 2001US-00837444.  
 PR 30-JAN-2002; 2002US-00958131.  
 PR 14-JUN-2002; 2002US-00171468.  
 PR 09-AUG-2002; 2002US-00225066.  
 PR 09-AUG-2002; 2002US-00225067.  
 PR 09-AUG-2002; 2002US-00225068.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 25-FEB-2003; 2003US-00374780.  
 XX (ZHAN/) ZHANG J.  
 PA (FROM/) FROMM M E.  
 PA (HEAR/) HEARD J E.  
 PA (RIEC/) RIECHMANN J L.  
 PA (ADAM/) ADAM L J.  
 PA (BROU/) BROUN P E.  
 PA (PINE/) PINEDA O.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J S.  
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 PA (JIANG/) JIANG C.  
 PA (SAMA/) SAMAHA R S.  
 PA (PIILG/) PILGRIM M L.  
 PA (CREE/) CREELMAN R A.  
 PA (DUBE/) DUBELL A N.  
 PA (RATC/) RATCLIFFE O.  
 PA (KIMI/) KIMIMOTO R.  
 PA (SHER/) SHERMAN B K.  
 XX Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE,  
 PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS,  
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kimimoto R,  
 PI Sherman BK;  
 XX WPI, 2004-225755/21.  
 DR N-PSDB; ADO01614.  
 XX  
 PT New transgenic plant, useful in developing phenotypes with altered or  
 PT improved characteristics or traits.  
 XX  
 PS Claim 1; SEQ ID NO 28; 213bp; English.  
 XX  
 CC The invention relates to a transgenic plant comprising a recombinant  
 CC polynucleotide having a polynucleotide sequence or its complementary  
 CC sequence comprising a sequence encoding a polypeptide, that initiates  
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,

Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588  
-ADO03527 or ADO03530-A DO03559. Also included are using a transgenic  
plant to grow a progeny plant, an expression cassette (comprising a  
constitutive, inducible or tissue-specific promoter and a recombinant  
polynucleotide described above), a host cell comprising the expression  
cassette, producing a modified plant having a modified trait, identifying  
a factor that is modulated by or interacts with a polypeptide encoded by  
the polynucleotide sequence and identifying at least one downstream  
CC polynucleotide sequence that is subject to a regulatory effect of any of  
the polypeptides encoded by the polynucleotide described above. The  
transgenic plant is useful for producing a plant that has an altered  
trait e.g. an enhanced tolerance to abiotic stress (increased tolerance  
to chilling, germination in cold conditions, freezing tolerance, tolerance  
to heat, tolerance to drought, tolerance to osmotic stress, tolerance to  
salt, tolerance to phosphate limitation, tolerance to potassium  
limitation, decreased sensitivity to nitrogen limitation), altered  
hormone sensitivity, reduced sensitivity to abscisic acid, an altered  
response to ethylene, disease resistance, altered susceptibility to  
bacteria, altered susceptibility to Pseudomonas syringae, altered  
susceptibility to Sclerotinia, altered sugar sensing, improved seed  
germination and seedling vigor, early flowering, late flowering, extended  
period of flowering, an inflorescence architectural change, a change in  
stem bifurcations, a lack of a shoot meristem, reduced meristem cell  
differentiation, altered phyllotaxy, altered branching pattern, reduced  
apical dominance, reduced trichome density, ectopic trichome development,  
altered trichome development, altered stem morphology, increased root  
growth, increased root hairs, altered seed development, altered cell  
proliferation/cell differentiation, premature senescence, delayed  
senescence, lethality, increased necrosis, an increase in seedling or  
plant size, decreased plant size, a change in leaf morphology, increased  
altered leaf development, increased leaf size and mass, glossy leaves,  
leaf cell expansion, change in seed morphology, altered seed coloration,  
increased seed size, decreased seed size, altered seed shape, change in  
leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid  
content, increased leaf insoluble sugars, decreased leaf insoluble  
sugars, increased leaf anthocyanins, an alteration of leaf fatty acid  
content, an alteration of leaf glucosinolate content, change in seed  
biochemistry, an increase in seed oil content, decrease in seed oil  
content, increase in seed fatty acid content, decrease in seed fatty acid  
content, increase in seed protein content, decrease in seed protein  
content, alteration in seed prenyl lipid content, increase in seed  
sterols, upregulation of genes involved in secondary metabolism, increase  
in root anthocyanins, increase in plant anthocyanins, and alteration in  
light response or shade avoidance. The present sequence represents a  
thalecress transcription factor of the invention.

SO Sequence 226 AA;

Query Match 9.4%; Score 19; DB 8; Length 226;  
Best Local Similarity 100.0%; Pred. No. 3e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 GVRRRPWGKFAAIEIRDPKK 120  
Db 94 GVRRRPWGKFAAIEIRDPKK 112

RESULT 14

ADN73807 standard; protein; 226 AA.

ADN73807;

15-JUL-2004 (first entry)

Thale cress protein repressed in E2Fa/Dpa expressing plants SegID 1702.

plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;

animal feed product; thale cress; cell wall biosynthesis;

nitrogen metabolism; carbon metabolism.

Arabidopsis thaliana.

XX  
PN WO2004035796-A2.  
XX  
XX 29-APR-2004.  
XX  
XX 20-OCT-2003; 2003WO-EP011658.  
PF  
XX 18-OCT-2002; 2002EP-00079408.  
PR  
XX  
XX (CROP-) CROPDESIGN NV.  
PA  
XX Inze D, De Veylder L, Vlieghe K;  
PI  
XX WPI; 2004-348466/32.  
DR  
XX N-PSDB; ADN73806.  
PT Altering plant characteristics, useful for producing plants for enzyme or  
pharmaceutical production comprises modifying in a plant, expression of  
one or more nucleic acids and/or modifying level or activity of one or  
more proteins.

Claim 1; SEQ ID NO 1702; 134dp; English.

PS This invention relates to a novel method for altering one or more plant  
characteristics. Specifically, it refers to identifying genes that are up  
- or down-regulated in transgenic plants overexpressing the heterodimeric  
CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to  
alter plant characteristics accordingly. The present invention describes  
CC generating transgenic plants for the production of growth regulators,  
enzymes, therapeutics, pharmaceuticals and animal feed products, where  
the altered plant characteristics are selected from increased yield or  
biomass, enhanced survival capacity, stress tolerance, plant architecture  
CC or physiology, altered endoreduplication, biochemistry, signal  
transduction, storage lipid mobilization and/or altered photosynthesis,  
each relative to the corresponding wild type plants. Accordingly, these  
sequences can also be useful as positive or negative selectable markers  
CC during transformation of cells or tissues. The identified genes play a  
role in a variety of biological processes such as DNA replication, cell  
wall biosynthesis, nitrogen and/or carbon metabolism or they function as  
transcription factors. This polypeptide sequence is thale cress protein  
CC expressed by a gene repressed 1.3 fold or more in plants overexpressing  
the E2Fa/Dpa transcription factor, given in an exemplification of the  
invention.

SO Sequence 226 AA;

Query Match 9.4%; Score 19; DB 8; Length 226;  
Best Local Similarity 100.0%; Pred. No. 3e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 GVRRRPWGKFAAIEIRDPKK 120  
Db 94 GVRRRPWGKFAAIEIRDPKK 112

RESULT 15

AAV97227 standard; protein; 210 AA.

AAV97227;

19-DEC-2000 (first entry)

Plant transcription factor AP2 DNA-binding domain polypeptide.

AP2; transcription factor; plant metabolism; metabolite; primary;

secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;

food coloring; flavouring; fragrance; antimicrobial; pathogenic;

insecticide; gene expression; modulation.

Catharanthus roseus.

WO200046383-A2.

XX 10-AUG-2000.  
 PD  
 XX  
 PF 07-FEB-2000; 2000MO-NL000075.  
 XX  
 PR 05-FEB-1999; 99DK-00000158.  
 PR 10-FEB-1999; 99US-0119388P.  
 XX  
 PA (UYLE-) RIJCKUNIV LEIDEN.  
 PI Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW,  
 XX  
 DR WPI; 2000-499380/44.  
 DR N-PSDB; AAA53744.  
 XX  
 PT Modulating level of metabolites and stress resistance in recombinant  
 PT cells for synthesis of plant metabolites such as alkaloids including  
 PT terpenoid indole alkaloids, by providing transcription factor to the  
 PT cell.  
 XX  
 PS Disclosure; Page 97; 101pp; English.  
 XX  
 CC Many plant secondary metabolites have value as pharmaceuticals, food  
 CC colourings, flavours and fragrances. Some plant secondary metabolites are  
 CC linked to plant or plant cell defence mechanisms and may confer to the  
 CC plant antimicrobial activity, protection against UV light, herbivores,  
 CC pathogens, insects and nematodes. Plant secondary metabolites such as  
 CC terpenoid indole alkaloids (TIA) represent a class of pharmaceutically  
 CC useful compounds which naturally occur in many plant species. New methods  
 CC are described which modulate the expression of one or more genes involved  
 CC in the biosynthesis of plant metabolites or their precursors in plant  
 CC cells. The method comprises inserting into a plant cell a sequence  
 CC encoding a transcription factor comprising an AP2 DNA-binding domain and  
 CC by modifying the expression of that transcription factor. Transcription  
 CC factors comprising an AP2 DNA-binding domain are useful as central  
 CC regulators of complex metabolite pathways involving numerous target genes  
 CC for such transcription factors. This means that the yield of commercially  
 CC valuable metabolite compounds can be enhanced and the tolerance of plants  
 CC towards exogenous stress factors can be influenced. The method is useful  
 CC for modulating the level of one or more metabolites. By providing a  
 CC transcription factor to the cell the level of the metabolite is enhanced  
 CC by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to  
 CC a cell to which the transcription factor is not provided  
 XX  
 SQ Sequence 210 AA;

Query Match 8.3%; Score 18; DB 3; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAEIRDPK 119  
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 DB 129 GVRRRPWGKFAEIRDPK 146

Search completed: February 27, 2005, 22:23:23  
 Job time : 166 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2005, 22:18:21 ; Search time 43 Seconds  
(without alignments)  
352.413 Million cell updates/sec

Title: US-09-890-782-6

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Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/aa/6B.COMB.pep:.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	17	8.4	60	US-09-300-672-9	Sequence 9, Appl
2	17	8.4	69	US-08-912-272-17	Sequence 17, Appl
3	17	8.4	69	US-09-026-039-17	Sequence 17, Appl
4	13	6.4	59	US-09-202-161B-25	Sequence 25, Appl
5	13	6.4	61	US-08-949-603-11	Sequence 11, Appl
6	13	6.4	61	US-08-706-270A-11	Sequence 11, Appl
7	13	6.4	61	US-08-949-580-11	Sequence 11, Appl
8	13	6.4	61	US-08-950-172A-11	Sequence 11, Appl
9	13	6.4	61	US-09-198-119C-11	Sequence 11, Appl
10	13	6.4	61	US-09-601-802D-11	Sequence 11, Appl
11	13	6.4	63	US-09-601-802D-134	Sequence 134, Appl
12	13	6.4	69	US-08-912-272-18	Sequence 18, Appl
13	13	6.4	69	US-08-912-272-20	Sequence 20, Appl
14	13	6.4	69	US-09-026-039-18	Sequence 18, Appl
15	13	6.4	69	US-09-026-039-20	Sequence 20, Appl
16	13	6.4	231	US-09-202-161B-1	Sequence 1, Appl
17	13	6.4	243	US-09-533-029-34	Sequence 34, Appl
18	13	6.4	268	US-09-533-029-18	Sequence 18, Appl
19	12	5.9	462	US-09-248-796A-14808	Sequence 14808, A
20	12	5.9	101	US-09-640-211A-921	Sequence 921, App
21	11	5.4	505	US-09-248-796A-14299	Sequence 14299, A
22	10	4.9	130	US-08-630-822A-90	Sequence 90, Appl
23	10	4.9	130	US-09-005-069-90	Sequence 90, Appl
24	10	4.9	130	US-09-171-156A-39	Sequence 39, Appl
25	10	4.9	130	US-09-004-730A-39	Sequence 39, Appl
26	10	4.9	130	US-08-981-799A-39	Sequence 39, Appl
27	10	4.9	141	US-09-828-303-17	Sequence 17, Appl

28	10	4.9	153	US-09-248-796A-28015	Sequence 28015, A
29	10	4.9	175	US-09-248-796A-23457	Sequence 23457, A
30	10	4.9	203	US-09-270-767-35326	Sequence 35326, A
31	10	4.9	203	US-09-270-767-50543	Sequence 50543, A
32	10	4.9	246	US-09-185-160-7	Sequence 7, Appl
33	10	4.9	249	US-09-248-796A-27128	Sequence 27128, A
34	10	4.9	256	US-09-485-529-5	Sequence 5, Appl
35	10	4.9	258	US-09-485-529-20	Sequence 20, Appl
36	10	4.9	266	US-09-248-796A-14280	Sequence 14280, A
37	10	4.9	273	US-09-248-796A-25975	Sequence 25975, A
38	10	4.9	289	US-09-270-767-60136	Sequence 60136, A
39	10	4.9	321	US-09-248-796A-14273	Sequence 14273, A
40	10	4.9	349	US-09-162-524-3	Sequence 3, Appl
41	10	4.9	367	US-08-213-419B-15	Sequence 15, Appl
42	10	4.9	379	US-09-270-767-34013	Sequence 34013, A
43	10	4.9	379	US-09-270-767-49230	Sequence 49230, A
44	10	4.9	382	US-08-213-419B-19	Sequence 19, Appl
45	10	4.9	408	US-09-802-213-9	Sequence 9, Appl

#### ALIGNMENTS

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RESULT 1
US-09-300-672-9
; Sequence 9, Application US/09300672
; Patent No. 6248937
; GENERAL INFORMATION:
; APPLICANT: Finkelstein, Ruth R.
; APPLICANT: Lynch, Tim
; APPLICANT: Goodman, Howard M.
; APPLICANT: Wang, Ming-Ji
; TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,
; FILE OF INVENTION: QUALITY AND COLD-TOLERANCE
; FILE REFERENCE: 480.89 (HV)
; CURRENT APPLICATION NUMBER: US/09/300,672
; CURRENT FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Ap2 domain protein
US-09-300-672-9

Query Match      8.4%; Score 17; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 9e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAIRIDP 118
Db      3 GVRRRPWGKFAIRIDP 19

RESULT 2
US-08-912-272-17
; Sequence 17, Application US/08912272
; Patent No. 6093874
; GENERAL INFORMATION:
; APPLICANT: Jofuku, K. Diane
; APPLICANT: Okamoto, Jack K.
; TITLE OF INVENTION: Methods for Improving Seeds
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/912,272
/ FILING DATE: 15-AUG-1997
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/879,827
/ FILING DATE: 20-JUN-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/700,152
/ FILING DATE: 20-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Baetian, Kevin L.
/ REGISTRATION NUMBER: 34,774
/ REFERENCE/DOCKET NUMBER: 023070-067220US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 69 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..69
/ OTHER INFORMATION: /note="AP2 domain within tobacco
/ OTHER INFORMATION: EREBP-1"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 36..51
/ OTHER INFORMATION: /note="putative EREBP-1 amphipathic
/ OTHER INFORMATION: alpha-helix"
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US-08-912-272-17

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Best local Similarity 100.0%; Pred. No. 1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAAEIRDP 118
      |||
Db      6 GVRRRPWGKFAAEIRDP 22

RESULT 3
US-09-026-039-17
/ Sequence 17, Application US/09026039
/ Patent No. 6329567
/ GENERAL INFORMATION:
/ APPLICANT: Jofuku, K. Diane
/ APPLICANT: Okamoto, Jack K.
/ TITLE OF INVENTION: Methods for Improving Seeds
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
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/ APPLICATION NUMBER: US/09/026,039
/ FILING DATE: 19-FEB-1998
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 08/912,272
/ FILING DATE: 15-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/879,827
/ FILING DATE: 20-JUN-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/700,152
/ FILING DATE: 20-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Baetian, Kevin L.
/ REGISTRATION NUMBER: 34,774
/ REFERENCE/DOCKET NUMBER: 023070-067230US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 69 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..69
/ OTHER INFORMATION: /note="AP2 domain within tobacco
/ OTHER INFORMATION: EREBP-1"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 36..51
/ OTHER INFORMATION: /note="putative EREBP-1 amphipathic
/ OTHER INFORMATION: alpha-helix"
/
US-09-026-039-17

Query Match      8.4%; Score 17; DB 3; Length 69;
Best local Similarity 100.0%; Pred. No. 1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAAEIRDP 118
      |||
Db      6 GVRRRPWGKFAAEIRDP 22

RESULT 4
US-09-202-161B-25
/ Sequence 25, Application US/09202161B
/ Patent No. 665353
/ GENERAL INFORMATION:
/ APPLICANT: Purdue Research Foundation
/ TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
/ FILE REFERENCE: 7024-371
/ CURRENT APPLICATION NUMBER: US/09/202,161B
/ CURRENT FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: PCT/US97/10382
/ PRIOR FILING DATE: 1997-06-12
/ PRIOR APPLICATION NUMBER: 60/046,494
/ PRIOR FILING DATE: 1997-05-14
/ PRIOR APPLICATION NUMBER: 60/019,633
/ PRIOR FILING DATE: 1996-06-12
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: ASCII
/ SEQ ID NO 25
/ LENGTH: 59
/ TYPE: PRT
/ ORGANISM: Lycopersicon esculentum
/
US-09-202-161B-25

Query Match      6.4%; Score 13; DB 4; Length 59;
Best local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      106 RFWGKFAAEIRDP 118
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Db 8 RFWGKFAAIRDP 20

## RESULT 5

US-08-949-603-11  
; Sequence 11, Application US/08949603  
; Patent No. 5891859  
; GENERAL INFORMATION:  
; APPLICANT: Michael F. Thomashow and  
; APPLICANT: Eric J. Stockinger  
; TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
; TITLE OF INVENTION: WHICH REGULATES COLD AND  
; TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48864  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS 5.00  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/949,603  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/706,270  
; FILING DATE: September 4, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ian C. McLeod  
; REGISTRATION NUMBER: 20,931  
; REFERENCE/DOCKET NUMBER: MSU 4.1-384  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 347-4100  
; TELEFAX: (517) 347-4103  
; TELEX: No. 5891859e  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61  
; TYPE: Amino Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Polypeptide  
; HYPOTHEICAL: No  
; ANTI-SENSE: No  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM: Tobacco  
; STRAIN:  
; INDIVIDUAL ISOLATE: N/A  
; DEVELOPMENTAL STAGE: N/A  
; HAPLOTYPE: N/A  
; TISSUE TYPE: N/A  
; CELL TYPE: N/A  
; CELL LINE: N/A  
; ORGANELLE: N/A  
; IMMEDIATE SOURCE: N/A  
; POSITION IN GENOME: N/A  
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; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD: sequencing  
; OTHER INFORMATION: Figure 2D  
; PUBLICATION INFORMATION:  
; US-08-949-603-11

Query Match 6.4%; Score 13; DB 2; Length 61;

Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 RFWGKFAAIRDP 118

Db 8 RFWGKFAAIRDP 20

## RESULT 6

US-08-706-270A-11  
; Sequence 11, Application US/08706270A  
; Patent No. 5892009  
; GENERAL INFORMATION:  
; APPLICANT: Michael F. Thomashow and  
; APPLICANT: Eric J. Stockinger  
; TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
; TITLE OF INVENTION: WHICH REGULATES COLD AND  
; TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48864  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS 5.00  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/706,270A  
; FILING DATE: September 4, 1996  
; CLASSIFICATION: 800  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ian C. McLeod  
; REGISTRATION NUMBER: 20,931  
; REFERENCE/DOCKET NUMBER: MSU 4.1-310  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 347-4100  
; TELEFAX: (517) 347-4103  
; TELEX: No. 5892009e  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61  
; TYPE: Amino Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Polypeptide  
; HYPOTHEICAL: No  
; ANTI-SENSE: No  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM: Tobacco  
; STRAIN:  
; INDIVIDUAL ISOLATE: N/A  
; DEVELOPMENTAL STAGE: N/A  
; HAPLOTYPE: N/A  
; TISSUE TYPE: N/A  
; CELL TYPE: N/A  
; CELL LINE: N/A  
; ORGANELLE: N/A  
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; POSITION IN GENOME: N/A  
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; LOCATION:  
; IDENTIFICATION METHOD: sequencing

OTHER INFORMATION: Figure 2D  
PUBLICATION INFORMATION:  
US-08-706-270A-11

Query Match 6.4%; Score 13; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 RFWGKFAAIRDP 118  
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Db 8 RFWGKFAAIRDP 20

RESULT 7  
US-08-949-580-11  
; Sequence 11, Application US/08949580  
; Patent No. 5929305  
; GENERAL INFORMATION:  
; APPLICANT: Michael F. Thomashow and  
; APPLICANT: Eric J. Stockinger  
; TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
; TITLE OF INVENTION: WHICH REGULATES COLD AND  
; TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48864  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS 5.00  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/949,580  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/706,270  
; FILING DATE: September 4, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ian C. McLeod  
; REGISTRATION NUMBER: 20,931  
; REFERENCE/DOCKET NUMBER: MSU 4.1-383  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 347-4100  
; TELEFAX: (517) 347-4103  
; TELEX: No. 5929305e  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61  
; TYPE: Amino Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Polypeptide  
; HYPOTHETICAL: No  
; ANTI-SENSE: No  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM: Tobacco  
; STRAIN:  
; INDIVIDUAL ISOLATE: N/A  
; DEVELOPMENTAL STAGE: N/A  
; HAPLOTYPE: N/A  
; TISSUE TYPE: N/A  
; CELL TYPE: N/A  
; CELL LINE: N/A  
; ORGANELLE: N/A  
; IMMEDIATE SOURCE: N/A

POSITION IN GENOME: N/A  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD: sequencing  
PUBLICATION INFORMATION:  
US-08-949-580-11

Query Match 6.4%; Score 13; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 RFWGKFAAIRDP 118  
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Db 8 RFWGKFAAIRDP 20

RESULT 8  
US-08-950-172A-11  
; Sequence 11, Application US/08950172A  
; Patent No. 5965705  
; GENERAL INFORMATION:  
; APPLICANT: Michael F. Thomashow and  
; APPLICANT: Eric J. Stockinger  
; TITLE OF INVENTION: DNA AND ENCODED PROTEIN  
; TITLE OF INVENTION: WHICH REGULATES COLD AND  
; TITLE OF INVENTION: DEHYDRATION REGULATED GENES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48864  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS 5.00  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/950,172A  
; FILING DATE: 10/14/1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/949,580  
; FILING DATE: October 14, 1997  
; APPLICATION NUMBER: 08/706,270  
; FILING DATE: September 4, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ian C. McLeod  
; REGISTRATION NUMBER: 20,931  
; REFERENCE/DOCKET NUMBER: MSU 4.1-383  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 347-4100  
; TELEFAX: (517) 347-4103  
; TELEX: No. 5965705e  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61  
; TYPE: Amino Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Polypeptide  
; HYPOTHETICAL: No  
; ANTI-SENSE: No  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM: Tobacco  
; STRAIN:  
; INDIVIDUAL ISOLATE: N/A

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; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELL: N/A
; IMMEDIATE SOURCE: N/A
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: Figure 2D
; PUBLICATION INFORMATION:
US-08-950-172A-11

Query Match      6.4%; Score 13; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      106 RFWGKFAAEIRDP 118
Db      8 RFWGKFAAEIRDP 20

RESULT 9
US-09-198-119C-11
; Sequence 11, Application US/09198119C
; Patent No. 6417428
; GENERAL INFORMATION:
; APPLICANT: Thomashow, Michael
; APPLICANT: Stockinger, Eric
; APPLICANT: Jaglo-Ottoesen, Kirsten
; APPLICANT: Gilmour, Sarah
; APPLICANT: Zarka, Daniel
; APPLICANT: Jiang, Cai-Zhong
; TITLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance
; FILE REFERENCE: 19117, 713 Seq List
; CURRENT APPLICATION NUMBER: US/09/198,119C
; CURRENT FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 08/706,270
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/018,233
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/017,816
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,235
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/017,575
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,227
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,234
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-198-119C-11

Query Match      6.4%; Score 13; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      106 RFWGKFAAEIRDP 118
Db      8 RFWGKFAAEIRDP 20

RESULT 10
US-09-601-802D-11
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; Sequence 11, Application US/09601802D
; Patent No. 6706866
; GENERAL INFORMATION:
; APPLICANT: Thomashow, Michael
; APPLICANT: Stockinger, Eric
; APPLICANT: Jaglo-Ottoesen, Kirsten
; APPLICANT: Gilmour, Sarah
; APPLICANT: Zarka, Daniel
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Zhang, James
; APPLICANT: Haake, Volker
; TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
; FILE REFERENCE: 51442000201/MB10029
; CURRENT APPLICATION NUMBER: US/09/601,802D
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/018,233
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/017,816
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/018,235
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/017,575
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/017,575
; PRIOR FILING DATE: 1998-02-03

US-09-601-802D-11

Query Match      6.4%; Score 13; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      106 RFWGKFAAEIRDP 118
Db      8 RFWGKFAAEIRDP 20

RESULT 11
US-09-601-802D-134
; Sequence 134, Application US/09601802D
; Patent No. 6706866
; GENERAL INFORMATION:
; APPLICANT: Thomashow, Michael
; APPLICANT: Stockinger, Eric
; APPLICANT: Jaglo-Ottoesen, Kirsten
; APPLICANT: Gilmour, Sarah
; APPLICANT: Zarka, Daniel
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Zhang, James
; APPLICANT: Haake, Volker
; TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
; FILE REFERENCE: 51442000201/MB10029
; CURRENT APPLICATION NUMBER: US/09/601,802D
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/018,233
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/017,816
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/018,235
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/017,575
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: 09/017,575
; PRIOR FILING DATE: 1998-02-03
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;; PRIOR APPLICATION NUMBER: 09/018,227  
;; PRIOR FILING DATE: 1998-02-03  
;; PRIOR APPLICATION NUMBER: 09/018,234  
;; PRIOR FILING DATE: 1998-02-03  
;; PRIOR APPLICATION NUMBER: 09/198,119  
;; PRIOR FILING DATE: 1998-11-23  
;; NUMBER OF SEQ ID NOS: 259  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 134  
;; LENGTH: 63  
;; TYPE: PRT  
;; ORGANISM: Nicotiana tabacum  
US-09-601-802D-134

Query Match 6.4%; Score 13; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RFWGKFAAEIRDP 118  
Db 10 RFWGKFAAEIRDP 22

RESULT 12  
US-08-912-272-18  
; Sequence 18, Application US/08912272  
; Patent No. 6093874  
; GENERAL INFORMATION:  
; APPLICANT: Jofuku, K. Diane  
; APPLICANT: Okamoto, Jack K.  
; TITLE OF INVENTION: Methods for Improving Seeds  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,272  
; FILING DATE: 15-AUG-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/879,827  
; FILING DATE: 20-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/700,152  
; FILING DATE: 20-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Basilian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-067220US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..69  
; OTHER INFORMATION: /note="Ap2 domain within tobacco  
; OTHER INFORMATION: EREBP-2"

;; FEATURE:  
;; NAME/KEY: Region  
;; LOCATION: 35..51  
;; OTHER INFORMATION: /note="putative EREBP-2 amphipathic  
;; OTHER INFORMATION: alpha-helix"  
US-08-912-272-18

Query Match 6.4%; Score 13; DB 3; Length 69;  
Best Local Similarity 100.0%; Pred. No. 6.8e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RFWGKFAAEIRDP 118  
Db 10 RFWGKFAAEIRDP 22

RESULT 13  
US-08-912-272-20  
; Sequence 20, Application US/08912272  
; Patent No. 6093874  
; GENERAL INFORMATION:  
; APPLICANT: Jofuku, K. Diane  
; APPLICANT: Okamoto, Jack K.  
; TITLE OF INVENTION: Methods for Improving Seeds  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,272  
; FILING DATE: 15-AUG-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/879,827  
; FILING DATE: 20-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/700,152  
; FILING DATE: 20-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Basilian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-067220US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..69  
; OTHER INFORMATION: /note="Ap2 domain within tobacco  
; OTHER INFORMATION: EREBP-4"  
; NAME/KEY: Region  
; LOCATION: 35..51  
; OTHER INFORMATION: /note="putative EREBP-4 amphipathic  
; OTHER INFORMATION: alpha-helix"  
US-08-912-272-20

Query Match 6.4%; Score 13; DB 3; Length 69;  
Best Local Similarity 100.0%; Pred. No. 6.8e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAEIRDP 118  
Db 10 RPKGKFAEIRDP 22

## RESULT 14

US-09-026-039-18  
; Sequence 18; Application US/09026039  
; Patent No. 6329567  
; GENERAL INFORMATION:  
; APPLICANT: Jofuku, K. Diane  
; APPLICANT: Okamuro, Jack K.  
; TITLE OF INVENTION: Methods for Improving Seeds  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,039  
; FILING DATE: 19-FEB-1998  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,272  
; FILING DATE: 15-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/879,827  
; FILING DATE: 20-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/700,152  
; FILING DATE: 20-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-067230US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..69  
; OTHER INFORMATION: /note="AP2 domain within tobacco  
; OTHER INFORMATION: EREBP-2"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 35..51  
; OTHER INFORMATION:  
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; OTHER INFORMATION: alpha-helix"  
US-09-026-039-18

Query Match 6.4%; Score 13; DB 3; Length 69;  
Best Local Similarity 100.0%; Pred. No. 6.8e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAEIRDP 118  
Db 10 RPKGKFAEIRDP 22

## RESULT 15

US-09-026-039-20  
; Sequence 20; Application US/09026039  
; Patent No. 6329567  
; GENERAL INFORMATION:  
; APPLICANT: Jofuku, K. Diane  
; APPLICANT: Okamuro, Jack K.  
; TITLE OF INVENTION: Methods for Improving Seeds  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,039  
; FILING DATE: 19-FEB-1998  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,272  
; FILING DATE: 15-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/879,827  
; FILING DATE: 20-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/700,152  
; FILING DATE: 20-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-067230US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..69  
; OTHER INFORMATION: /note="AP2 domain within tobacco  
; OTHER INFORMATION: EREBP-4"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 35..51  
; OTHER INFORMATION:  
; OTHER INFORMATION: /note="putative EREBP-4 amphipathic  
; OTHER INFORMATION: alpha-helix"  
US-09-026-039-20

Query Match 6.4%; Score 13; DB 3; Length 69;  
Best Local Similarity 100.0%; Pred. No. 6.8e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAEIRDP 118  
Db 10 RPKGKFAEIRDP 22

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Job time : 44 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 27, 2005, 22:26:32 ; Search time 129 Seconds

(without alignments)  
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Title: US-09-890-782-6

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## SUMMARIES

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4	23	11.3	203	US-10-425-114-36689	Sequence 36689, A
5	19	9.4	156	US-10-424-599-208822	Sequence 208822, A
6	19	9.4	202	US-10-424-599-175489	Sequence 175489, A
7	19	9.4	226	US-10-425-068-128	Sequence 128, App
8	19	9.4	226	US-10-374-780A-6	Sequence 6, Appl
9	19	9.4	226	US-10-412-699B-28	Sequence 28, Appl
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11	17	8.4	139	US-09-934-455-6	Sequence 6, Appl
12	17	8.4	139	US-10-225-068-46	Sequence 46, Appl
13	17	8.4	139	US-10-225-066A-170	Sequence 170, App

14	17	8.4	139	US-10-374-780A-332	Sequence 332, App
15	17	8.4	152	US-10-425-114-41831	Sequence 41831, A
16	17	8.4	178	US-10-424-599-174805	Sequence 174805, A
17	17	8.4	201	US-10-225-066A-788	Sequence 788, App
18	17	8.4	201	US-10-374-780A-2230	Sequence 2230, App
19	17	8.4	201	US-10-412-699B-50	Sequence 50, Appl
20	17	8.4	201	US-10-412-699B-1726	Sequence 1726, Ap
21	17	8.4	207	US-10-278-536-54	Sequence 54, Appl
22	17	8.4	207	US-10-412-699B-54	Sequence 54, Appl
23	17	8.4	209	US-10-424-599-172483	Sequence 172483, A
24	17	8.4	214	US-10-425-114-37800	Sequence 37800, A
25	17	8.4	222	US-10-425-114-39220	Sequence 39220, A
26	17	8.4	224	US-10-425-114-41699	Sequence 41699, A
27	17	8.4	282	US-10-374-780A-503	Sequence 503, App
28	17	8.4	299	US-10-374-780A-1157	Sequence 1157, App
29	17	8.4	299	US-10-412-699B-1360	Sequence 1360, App
30	17	8.4	299	US-10-437-963-156010	Sequence 156010, A
31	17	8.4	1040	US-10-437-963-156030	Sequence 120630, A
32	16	7.9	112	US-10-424-599-247090	Sequence 247090, A
33	16	7.9	131	US-10-062-254-220	Sequence 220, App
34	16	7.9	131	US-10-374-780A-1736	Sequence 1736, App
35	16	7.9	150	US-10-424-599-223956	Sequence 223956, A
36	16	7.9	157	US-10-424-599-149169	Sequence 149169, A
37	16	7.9	218	US-09-934-455-192	Sequence 192, App
38	16	7.9	218	US-10-225-068-210	Sequence 210, App
39	16	7.9	218	US-10-225-066A-58	Sequence 58, Appl
40	16	7.9	218	US-10-225-067-70	Sequence 70, Appl
41	16	7.9	218	US-10-374-780A-252	Sequence 252, App
42	16	7.9	218	US-10-412-699B-800	Sequence 800, App
43	16	7.9	218	US-10-424-599-154832	Sequence 154832, A
44	16	7.9	220	US-10-425-114-40926	Sequence 40926, A
45	16	7.9	224	US-10-424-599-160662	Sequence 160662, A

## ALIGNMENTS

RESULT 1  
US-10-425-114-52229  
; Sequence 52229, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313) B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ. ID NOS: 73128  
; SEQ. ID NO 52229  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700869231\_FLI.pep  
US-10-425-114-52229  
Query Match 11.3%; Score 23; DB 15; Length 137;  
Best Local Similarity 100.0%; Pred. No. 7.4e-13;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 102 GVRRRPMGKFAARIRDPKXKGR 124  
DB 49 GVRRRPMGKFAARIRDPKXKGR 71  
RESULT 2  
US-10-424-599-214399

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; Sequence 214399, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214399
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3562C.1.pep
US-10-424-599-214399

Query Match          11.3%; Score 23; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.8e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAAEIRDPKKGSR 124
DB      58 GVRRRPWGKFAAEIRDPKKGSR 80

RESULT 3
US-10-424-599-214365
; Sequence 214365, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214365
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3559C.1.pep
US-10-424-599-214365

Query Match          11.3%; Score 23; DB 15; Length 199;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAAEIRDPKKGSR 124
DB      111 GVRRRPWGKFAAEIRDPKKGSR 133

RESULT 4
US-10-425-114-36689
; Sequence 36689, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
```

```
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36689
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3093-015-B5_F1.1.pep
US-10-425-114-36689

Query Match          11.3%; Score 23; DB 15; Length 203;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAAEIRDPKKGSR 124
DB      115 GVRRRPWGKFAAEIRDPKKGSR 137

RESULT 5
US-10-424-599-208822
; Sequence 208822, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 208822
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_30595C.1.pep
US-10-424-599-208822

Query Match          9.4%; Score 19; DB 15; Length 156;
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAAEIRDPK 120
DB      69 GVRRRPWGKFAAEIRDPK 87

RESULT 6
US-10-424-599-175489
; Sequence 175489, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 175489
; LENGTH: 202
; TYPE: PRT
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; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_129485C.1.pap
US-10-424-599-175489
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Query Match          9.4%; Score 19; DB 15; Length 202;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      102 GVRRRPMGKFAAIRDPKK 120
          |||
          79 GVRRRPMGKFAAIRDPKK 97
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RESULT 7
US-10-225-068-128
; Sequence 128, Application US/10225068
; Publication No. US20030217363A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Adam, Luc J.
; APPLICANT: Dubell, Arnold T.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Brown, Pierre E.
; TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
; FILE REFERENCE: 51444202040
; CURRENT APPLICATION NUMBER: US/10/225,068
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (89)...(157)
; OTHER INFORMATION: Conserved domain
US-10-225-068-128
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Query Match          9.4%; Score 19; DB 15; Length 226;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      102 GVRRRPMGKFAAIRDPKK 120
          |||
          94 GVRRRPMGKFAAIRDPKK 112
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```
RESULT 8
US-10-374-780A-6
; Sequence 6, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
```

```
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: Brown, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G22 (conserved domain in AA coordinates: 89-157)
US-10-374-780A-6

Query Match          9.4%; Score 19; DB 15; Length 226;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      102 GVRRRPMGKFAAIRDPKK 120
          |||
          94 GVRRRPMGKFAAIRDPKK 112
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```
RESULT 9
US-10-412-699B-28
; Sequence 28, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Brown, Pierre E.
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: Dubell, Arnold N.
```

```
APPLICANT: Ratcliffe, Oliver
APPLICANT: Kumimoto, Roderick
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MBI-0048CIP
CURRENT APPLICATION NUMBER: US/10/412,699B
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/532,591
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,648
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/713,994
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/819,142
PRIOR FILING DATE: 2001-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: PatentIn version 3.2
SEQ ID NO 28
LENGTH: 226
TYPE: PRT
ORGANISM: Arabidopsis thaliana
OTHER INFORMATION: G22
US-10-412-699B-28
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Query Match          9.4%; Score 19; DB 15; Length 226;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      102 GVRRRPWGKFAAEIRDPK 120
      |||||
DB      94 GVRRRPWGKFAAEIRDPK 112
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RESULT 10
US-10-374-780A-1737
Sequence 1737, Application US/10374780A
Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
APPLICANT: Creelman, Robert A
APPLICANT: Ratcliffe, Oliver
APPLICANT: Adam, Luc J
APPLICANT: Reuber, T. Lynne
APPLICANT: Keddie, James E
APPLICANT: Brown, Pierre E
APPLICANT: Pilgrim, Marsha L
APPLICANT: Dubell III, Arnold T
APPLICANT: Pineda, Omaira
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
PRIOR FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
```

```
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1737
LENGTH: 124
TYPE: PRT
ORGANISM: Oryza sativa japonica
FEATURE:
OTHER INFORMATION: G3383 Orthologous to G1792
US-10-374-780A-1737
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Query Match          8.4%; Score 17; DB 15; Length 124;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      102 GVRRRPWGKFAAEIRDP 118
      |||||
DB      15 GVRRRPWGKFAAEIRDP 31
```

```
RESULT 11
US-09-934-455-6
Sequence 6, Application US/09934455
Publication No. US20030121070A1
GENERAL INFORMATION:
APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Keddie, James
APPLICANT: Pilgrim, Marsha
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, Lynne
APPLICANT: Riechmann, Jose Luis
APPLICANT: Yu, Guo-Liang
APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 139
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-934-455-6
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Query Match          8.4%; Score 17; DB 10; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      102 GVRRRPWGKFAAIRDP 118
      |||||
Db      22 GVRRRPWGKFAAIRDP 38

RESULT 12
US-10-225-066A-46
; Sequence 46, Application US/10225068
; Publication No. US20030217383A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Adam, Luc J.
; APPLICANT: Dubell, Arnold T.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pineda, Omalra
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Broun, Pierre E.
; TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
; FILE REFERENCE: 514442002040
; CURRENT APPLICATION NUMBER: US/10/225,068
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (17)...(85)
; OTHER INFORMATION: Conserved domain
US-10-225-066A-46

Query Match      8.4%; Score 17; DB 15; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAAIRDP 118
      |||||
Db      22 GVRRRPWGKFAAIRDP 38

RESULT 13
US-10-225-066A-170
; Sequence 170, Application US/10225066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omalra
; APPLICANT: YU, Guo-Liang

QY      102 GVRRRPWGKFAAIRDP 118
      |||||
Db      22 GVRRRPWGKFAAIRDP 38

RESULT 14
US-10-374-780A-332
; Sequence 332, Application US/10374780A
; Publication No. US2004001927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Pineda, Omalra
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068

APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI0036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-170

Query Match      8.4%; Score 17; DB 15; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ PRIOR FILING DATE: 2002-08-09  
/ NUMBER OF SEQ ID NOS: 2906  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 332  
/ LENGTH: 139  
/ TYPE: PRT  
/ ORGANISM: Arabidopsis thaliana  
/ FEATURE:  
/ OTHER INFORMATION: G1792 (conserved domain in aa coordinates: 17-85)  
US-10-374-780A-332

Query Match 8.4%; Score 17; DB 15; Length 139;  
Best Local Similarity 100.0%; Pred.No. 2.2e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAEIRDP 118  
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Db 22 GVRRRPWGKFAAEIRDP 38

## RESULT 15

US-10-425-114-41831  
/ Sequence 41831, Application US/10425114  
/ Publication No. US20040034888A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Liu, Jindong  
/ APPLICANT: Zhou, Yihua  
/ APPLICANT: Kovalic, David K.  
/ APPLICANT: Screen, Steven E  
/ APPLICANT: Tabaska, Jack E  
/ APPLICANT: Cao, Yongwei  
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
/ FILE REFERENCE: 38-21(5313)B  
/ CURRENT APPLICATION NUMBER: US/10/425,114  
/ CURRENT FILING DATE: 2003-04-28  
/ NUMBER OF SEQ ID NOS: 73128  
/ SEQ ID NO 41831  
/ LENGTH: 152  
/ TYPE: PRT  
/ ORGANISM: Arabidopsis thaliana  
/ FEATURE:  
/ OTHER INFORMATION: Clone ID: LIB25-065-D10\_FLI.pep  
US-10-425-114-41831

Query Match 8.4%; Score 17; DB 15; Length 152;  
Best Local Similarity 100.0%; Pred.No. 2.4e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GVRRRPWGKFAAEIRDP 118  
|||  
Db 60 GVRRRPWGKFAAEIRDP 76

Search completed: February 27, 2005, 22:38:55  
Job time : 130 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2005, 22:17:56 / Search time 40 Seconds

(without alignments)  
488.300 Million cell updates/sec

Title: US-09-890-782-6

Perfect score: 203  
Sequence: 1 MEEETISVSDRFLSLIEH.....SSSSSSSSSENSGKRRRY 203

Scoring table: Oligo  
Gapop 60.0, Gapept 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Listing first 45 summaries

Database: PIR 79:\*

1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	9.4	226	2 T00409	ethylene-responsiv
2	17	8.4	207	2 T49897	transcription fact
3	17	8.4	236	2 T02432	ethylene-responsiv
4	16	7.9	277	2 T03927	DNA binding protei
5	14	6.9	268	2 T04787	hypothetical prote
6	13	6.4	225	2 A85196	ERBP-2 protein [l
7	13	6.4	233	2 T02590	DNA binding protei
8	13	6.4	234	2 T07686	transcription fact
9	13	6.4	263	2 T51989	ethylene responsiv
10	13	6.4	266	2 T51988	ethylene responsiv
11	13	6.4	281	2 T52189	ethylene responsiv
12	13	6.4	291	2 T02434	DNA binding protei
13	13	6.4	294	2 C84901	probable AP2 domai
14	13	6.4	300	2 T52020	ethylene responsiv
15	13	6.4	315	2 T47955	hypothetical prote
16	13	6.4	349	2 T41394	hypothetical serin
17	13	6.4	603	2 E71444	probable ERBP-4 -
18	12	5.9	236	2 B84718	hypothetical prote
19	12	5.9	244	2 B86197	hypothetical prote
20	12	5.9	262	2 T40941	hypothetical serin
21	12	5.9	303	2 T04541	hypothetical prote
22	11	5.4	297	2 E84731	hypothetical prote
23	11	5.4	468	2 A55476	protein kinase (EC
24	11	5.4	503	2 S63257	probable membrane
25	11	5.4	591	2 T19746	hypothetical prote
26	11	5.4	1341	2 S50366	probable membrane
27	11	5.4	1788	2 T31095	vitellogenin precu
28	11	5.4	1858	2 T18273	1-phosphatidylinos
29	11	5.4	1912	2 T29088	vitellinogenin I pre

30	10	4.9	135	2 T09876	dehydrin - upland
31	10	4.9	145	2 S04042	embryonic abundant
32	10	4.9	149	2 T23179	hypothetical prote
33	10	4.9	153	2 S67294	hypothetical prote
34	10	4.9	164	2 T16168	hypothetical prote
35	10	4.9	166	2 T07089	dehydrin - soybean
36	10	4.9	198	2 A94243	GLOF-C4 protein -
37	10	4.9	216	2 B66794	unknown protein F1
38	10	4.9	228	2 S19132	rab25 protein - ri
39	10	4.9	229	2 JC7219	nuclear protein SR
40	10	4.9	238	2 T52505	hypothetical prote
41	10	4.9	238	2 T32889	hypothetical prote
42	10	4.9	282	2 T21222	hypothetical prote
43	10	4.9	286	2 C61615	sericin MG-2 - gre
44	10	4.9	290	2 T21868	hypothetical prote
45	10	4.9	292	2 I51171	transcription fact

#### ALIGNMENTS

```
RESULT 1
T00409
ethylene-responsive transcription factor homolog T13E15.15 - Arabidopsis thaliana
N/Alternate names: hypothetical protein Atg244840
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C/Accession: T00409; D84883
R/Rounsley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mas
submitted to the EMBL Data Library, July 1997
A/Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.
A/Reference number: Z14146
A/Accession: T00409
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-226 <ROU>
A/Cross-references: UNIPROT:Q22167; EMBL:AC002388; NID:G3420042; PID:G2344900
A/Experimental source: cultivar Columbia
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shen, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
gues, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MIMD:20083487; PMID:10617197
A/Accession: D84883
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-226 <STO>
C/Cross-references: GB:AE002093; NID:G2344900; PIDN:AAC31840.1; GSPDB:GN00139
A/Accession: AC2944840; T13E15.15
A/Map position: 2

Query Match          9.4% Score 19; DB 2; Length 226;
Best Local Similarity 100.0%; Pred No. 1.4e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      102 GVRRRPWGKFAAIRDPRK 120
      |||||
Db      94 GVRRRPWGKFAAIRDPRK 112

RESULT 2
T49897
transcription factor-like protein - Arabidopsis thaliana
N/Alternate names: protein T211.290
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C/Accession: T49897
R/Devan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; L
submitted to the Protein Sequence Database, April 2000
A/Reference number: Z24493
A/Accession: T49897
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A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-207 <BEV>  
A:Cross-references: UNIPROT:Q9LY05; EMBL:AL163912; GSPDB:GN00063; ATSP:T211.290  
A:Experimental source: cultivar Columbia; BAC clone T211  
C:Genetics:  
A:Gene: ATSP:T211.290  
A:Map position: 5

Query Match 8.4%; Score 17; DB 2; Length 207;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 GVRRRPWGKFAAEIRDP 118  
|||  
Db 112 GVRRRPWGKFAAEIRDP 128

## RESULT 3

T02432  
ethylene-responsive transcription factor ERF1 - common tobacco  
C:Species: Nicotiana tabacum (common tobacco)  
C>Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T02432  
R:Ohme-Takagi, M.; Shinshi, H.  
Plant Cell 7, 173-182, 1995  
A:Title: Ethylene-inducible DNA binding proteins that interact with an ethylene response  
A:Reference number: Z14671; MUID:95276459; PMID:7756828  
A:Accession: T02432  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <OHM>  
A:Cross-references: UNIPROT:Q0476; EMBL:D38123; NID:9790359; PIDN:BA07321.1; PID:g1208  
A:Experimental source: strain BY4; tissue-type leaf

Query Match 8.4%; Score 17; DB 2; Length 236;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 GVRRRPWGKFAAEIRDP 118  
|||  
Db 107 GVRRRPWGKFAAEIRDP 123

## RESULT 4

T03927  
DNA binding protein S25-XPI - common tobacco  
C:Species: Nicotiana tabacum (common tobacco)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T03927  
R:Xu, P.; Ling, J.; Li, D.; Hasegawa, P.M.; Bressan, R.A.  
submitted to the EMBL Data Library, December 1996  
A:Reference number: Z15139  
A:Accession: T03927  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <XUP>  
A:Cross-references: UNIPROT:P93392; EMBL:U81157; NID:g1732405; PIDN:AA838748.1; PID:g173  
A:Experimental source: strain Wisconsin-38

Query Match 7.9%; Score 16; DB 2; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 GVRRRPWGKFAAEIRDP 117  
|||  
Db 94 GVRRRPWGKFAAEIRDP 109

RESULT 5  
T04787  
hypothetical protein F10M10.180 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T04787  
R:Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hohelsel, J.; Mewes, H.W.; Mayer,  
submitted to the Protein Sequence Database, February 1999  
A:Reference number: Z15384  
A:Accession: T04787  
A:Molecule type: DNA  
A:Residues: 1-268 <BEV>  
A:Cross-references: UNIPROT:Q9S206; EMBL:AL035521  
A:Experimental source: cultivar Columbia; BAC clone F10M10  
C:Genetics:  
A:Map position: 4  
A:Note: F10M10.180

Query Match 6.9%; Score 14; DB 2; Length 268;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 RPWKGKFAAEIRDP 119  
|||  
Db 142 RPWKGKFAAEIRDPK 155

## RESULT 6

A85196  
ERBP-2 protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: A85196  
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488; PMID:10617198  
A:Accession: A85196  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-225 <STO>  
A:Cross-references: GB:NC\_001268; NID:g5281024; PIDN:CA845963.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: d14785w  
A:Map position: 4

Query Match 6.4%; Score 13; DB 2; Length 225;  
Best Local Similarity 100.0%; Pred. No. 9.2e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 RPWKGKFAAEIRDP 118  
|||  
Db 111 RPWKGKFAAEIRDP 123

## RESULT 7

T02590  
DNA binding protein ERBP-2 - common tobacco  
C:Species: Nicotiana tabacum (common tobacco)  
C>Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T02590  
R:Ohme-Takagi, M.; Shinshi, H.  
Plant Cell 7, 173-182, 1995  
A:Title: Ethylene-inducible DNA binding proteins that interact with an ethylene response  
A:Reference number: Z14671; MUID:95276459; PMID:7756828  
A:Accession: T02590  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-233 <OHM>  
A:Cross-references: UNIPROT:Q0479; EMBL:D38126; NID:9790362; PIDN:BA07324.1; PID:g1208  
A:Experimental source: strain BY4; tissue-type leaf

Query Match 6.4%; Score 13; DB 2; Length 233;  
Best Local Similarity 100.0%; Pred. No. 9.5e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 RPWKGKFAAEIRDP 118

Db 105 RPKGKFAAEIRDP 117

## RESULT 8

T07686  
transcription factor Pt14 - tomato (fragment)  
C/Species: Lycopersicon esculentum (tomato)  
C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C/Accession: T07686  
R/Zhou, Y.; Tang, X.; Martin, G.B.  
submitted to the EMBL Data Library, July 1998  
A/Reference number: Z16094  
A/Accession: T07686  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-234 <ZHO>  
A/Cross-references: UNIPROT:Q04680; EMBL:U89255; NID:g3342210; PIDN:MAC50047.1; PID:g334  
C/Function:  
A/Description: transcription factor  
A/Note: binds the GCC box, present in the promoter region of genes encoding pathogenesis  
C/Keywords: DNA binding; transcription factor

Query Match 6.4%; Score 13; DB 2; Length 234;  
Best Local Similarity 100.0%; Pred. No. 9.9e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAAEIRDP 118  
Db 112 RPKGKFAAEIRDP 124

## RESULT 9

T51989  
ethylene responsive element binding factor 2 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C/Accession: T51989  
R/Fujimoto, S.Y.; Ohta, M.; Ueui, A.; Shinshi, H.; Ohme-Takagi, M.  
Plant Cell 12, 393-404, 2000  
A/Title: Arabidopsis ethylene responsive element binding factors act as transcriptional  
A/Reference number: Z25893  
A/Accession: T51989  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-243 <FUJ>  
A/Cross-references: UNIPROT:O80338; EMBL:AB008104; PIDN:BA32419.1  
C/Genetics:  
A/Gene: ERF-2

Query Match 6.4%; Score 13; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 9.9e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAAEIRDP 118  
Db 123 RPKGKFAAEIRDP 135

## RESULT 10

T51988  
ethylene responsive element binding factor 1 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 20-Oct-2000  
C/Accession: T51988  
R/Fujimoto, S.Y.; Ohta, M.; Ueui, A.; Shinshi, H.; Ohme-Takagi, M.  
Plant Cell 12, 393-404, 2000  
A/Title: Arabidopsis ethylene responsive element binding factors act as transcriptional  
A/Reference number: Z25893  
A/Accession: T51988  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-266 <FUJ>

A/Cross-references: EMBL:AB008103; PIDN:BA32418.1  
C/Genetics:  
A/Gene: ERF-1

Query Match 6.4%; Score 13; DB 2; Length 266;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAAEIRDP 118  
Db 152 RPKGKFAAEIRDP 164

## RESULT 11

T52189  
ethylene responsive element binding factor [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C/Accession: T52189  
R/Ueui, A.; Ohta, M.; Shinshi, H.; Ohme-Takagi, M.  
submitted to the EMBL Data Library, April 1998  
A/Description: Arabidopsis ethylene responsive element binding factor (AtERF5).  
A/Reference number: Z25994  
A/Accession: T52189  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-281 <USU>  
A/Cross-references: UNIPROT:O80387; EMBL:AB013301; PIDN:BA31525.1  
C/Genetics:  
A/Gene: ERF6

Query Match 6.4%; Score 13; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAAEIRDP 118  
Db 143 RPKGKFAAEIRDP 155

## RESULT 12

T02434  
DNA binding protein ERF6P-4 - common tobacco  
C/Species: Nicotiana tabacum (common tobacco)  
C/Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C/Accession: T02434  
R/Ohme-Takagi, M.; Shinshi, H.  
Plant Cell 7, 173-182, 1995  
A/Title: Ethylene-inducible DNA binding proteins that interact with an ethylene respons  
A/Reference number: Z14671; MUID:95276459; PMID:7756828  
A/Accession: T02434  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-291 <OHM>  
A/Cross-references: UNIPROT:Q40478; EMBL:J88125; NID:g7990361; PIDN:BA07323.1; PID:g120  
A/Experimental source: strain B14; tissue-type leaf  
C/Superfamily: Arabidopsis thaliana hypothetical protein T19P19.170

Query Match 6.4%; Score 13; DB 2; Length 291;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RPKGKFAAEIRDP 118  
Db 151 RPKGKFAAEIRDP 163

## RESULT 13

C84901  
probable AP2 domain transcription factor [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: C84901

R./lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentol, M.I.; Town, C.D.; Fujii, C.Y.;  
M. Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umeyam, L.; Tallon, L.  
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: AB4420; MUID:20083487; PMID:10617197  
A/Accession: C84901  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1294 <STO>  
A/Cross-references: UNIPROT:O82339; GB:AE002093; NID:93702318; PIDN:MAC62875.1; GSPDB:GN  
C/Genetics:  
A/Gene: AC2946310  
A/Map position: 2  
C/Superfamily: Arabidopsis thaliana hypothetical protein F15G16.20

Query Match 6.4%; Score 13; DB 2; Length 294;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RFWGKFAAETIRDP 118  
DB 105 RFWGKFAAETIRDP 117

## RESULT 14

T52020  
ethylene responsive element binding factor 5 [validated] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C/Accession: T52020  
R/Fujimoto, S.Y.; Ohta, M.; Usui, A.; Shinsui, H.; Ohme-Takagi, M.  
Plant Cell 12, 393-404, 2000  
A/Title: Arabidopsis ethylene responsive element binding factors act as transcriptional  
A/Reference number: Z25893  
A/Accession: T52020  
A/Status: Preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-300 <PUT>  
A/Cross-references: UNIPROT:O80341; EMBL:AB008107; PIDN:BAJ32422.1  
C/Genetics:  
A/Note: ATERF-5  
C/Function:  
A/Description: acts as a transcriptional activator for GCC box-dependent transcription

Query Match 6.4%; Score 13; DB 2; Length 300;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RFWGKFAAETIRDP 118  
DB 162 RFWGKFAAETIRDP 174

## RESULT 15

T47955  
hypothetical protein F15G16.20 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C/Accession: T47955  
R/De Haan, M.; Maarse, A.C.; Givelli, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet  
submitted to the Protein Sequence Database, January 2000  
A/Reference number: Z24480  
A/Accession: T47955  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-315 <DEH>  
A/Cross-references: UNIPROT:Q9W374; EMBL:AL132959  
A/Experimental source: cultivar Columbia; BAC clone F15G16  
C/Genetics:  
A/Map position: 3  
A/Note: F15G16.20  
C/Superfamily: Arabidopsis thaliana hypothetical protein F15G16.20

Query Match 6.4%; Score 13; DB 2; Length 315;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 RFWGKFAAETIRDP 118  
DB 111 RFWGKFAAETIRDP 123

Search completed: February 27, 2005, 22:27:10  
Job time : 41 secs